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(54) Title: **TRANSPORTERS AND ION CHANNELS**

(57) Abstract: The invention provides human transporters and ion channels (TRICH) and polynucleotides which identify and encode TRICH. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of TRICH.



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TRANSPORTERS AND ION CHANNELS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of transporters and ion channels
5 and to the use of these sequences in the diagnosis, treatment, and prevention of transport, neurological, muscle, immunological, and cell proliferative disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels.

10 BACKGROUND OF THE INVENTION

Eukaryotic cells are surrounded and subdivided into functionally distinct organelles by hydrophobic lipid bilayer membranes which are highly impermeable to most polar molecules. Cells and organelles require transport proteins to import and export essential nutrients and metal ions including K^+ , NH_4^+ , P_i , SO_4^{2-} , sugars, and vitamins, as well as various metabolic waste products. Transport
15 proteins also play roles in antibiotic resistance, toxin secretion, ion balance, synaptic neurotransmission, kidney function, intestinal absorption, tumor growth, and other diverse cell functions (Griffith, J. and C. Sansom (1998) The Transporter Facts Book, Academic Press, San Diego CA, pp. 3-29). Transport can occur by a passive concentration-dependent mechanism, or can be linked to an energy source such as ATP hydrolysis or an ion gradient. Proteins that function in transport include carrier proteins, which
20 bind to a specific solute and undergo a conformational change that translocates the bound solute across the membrane, and channel proteins, which form hydrophilic pores that allow specific solutes to diffuse through the membrane down an electrochemical solute gradient.

Carrier proteins which transport a single solute from one side of the membrane to the other are called uniporters. In contrast, coupled transporters link the transfer of one solute with
25 simultaneous or sequential transfer of a second solute, either in the same direction (symport) or in the opposite direction (antiport). For example, intestinal and kidney epithelium contains a variety of symporter systems driven by the sodium gradient that exists across the plasma membrane. Sodium moves into the cell down its electrochemical gradient and brings the solute into the cell with it. The sodium gradient that provides the driving force for solute uptake is maintained by the ubiquitous
30 Na^+/K^+ ATPase system. Sodium-coupled transporters include the mammalian glucose transporter (SGLT1), iodide transporter (NIS), and multivitamin transporter (SMVT). All three transporters have twelve putative transmembrane segments, extracellular glycosylation sites, and cytoplasmically-oriented N- and C-termini. NIS plays a crucial role in the evaluation, diagnosis, and treatment of various thyroid pathologies because it is the molecular basis for radioiodide thyroid-imaging

techniques and for specific targeting of radioisotopes to the thyroid gland (Levy, O. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:5568-5573). SMVT is expressed in the intestinal mucosa, kidney, and placenta, and is implicated in the transport of the water-soluble vitamins, e.g., biotin and pantothenate (Prasad, P.D. et al. (1998) *J. Biol. Chem.* 273:7501-7506).

5 One of the largest families of transporters is the major facilitator superfamily (MFS), also called the uniporter-symporter-antiporter family. MFS transporters are single polypeptide carriers that transport small solutes in response to ion gradients. Members of the MFS are found in all classes of living organisms, and include transporters for sugars, oligosaccharides, phosphates, nitrates, nucleosides, monocarboxylates, and drugs. MFS transporters found in eukaryotes all have a structure
10 comprising 12 transmembrane segments (Pao, S.S. et al. (1998) *Microbiol. Molec. Biol. Rev.* 62:1-34). The largest family of MFS transporters is the sugar transporter family, which includes the seven glucose transporters (GLUT1-GLUT7) found in humans that are required for the transport of glucose and other hexose sugars. These glucose transport proteins have unique tissue distributions and physiological functions. GLUT1 provides many cell types with their basal glucose requirements and
15 transports glucose across epithelial and endothelial barrier tissues; GLUT2 facilitates glucose uptake or efflux from the liver; GLUT3 regulates glucose supply to neurons; GLUT4 is responsible for insulin-regulated glucose disposal; and GLUT5 regulates fructose uptake into skeletal muscle. Defects in glucose transporters are involved in a recently identified neurological syndrome causing infantile seizures and developmental delay, as well as glycogen storage disease, Fanconi-Bickel
20 syndrome, and non-insulin-dependent diabetes mellitus (Mueckler, M. (1994) *Eur. J. Biochem.* 219:713-725; Longo, N. and L.J. Elsas (1998) *Adv. Pediatr.* 45:293-313).

Monocarboxylate anion transporters are proton-coupled symporters with a broad substrate specificity that includes L-lactate, pyruvate, and the ketone bodies acetate, acetoacetate, and beta-hydroxybutyrate. At least seven isoforms have been identified to date. The isoforms are predicted
25 to have twelve transmembrane (TM) helical domains with a large intracellular loop between TM6 and TM7, and play a critical role in maintaining intracellular pH by removing the protons that are produced stoichiometrically with lactate during glycolysis. The best characterized H⁺-monocarboxylate transporter is that of the erythrocyte membrane, which transports L-lactate and a wide range of other aliphatic monocarboxylates. Other cells possess H⁺-linked monocarboxylate transporters with differing
30 substrate and inhibitor selectivities. In particular, cardiac muscle and tumor cells have transporters that differ in their K_m values for certain substrates, including stereoselectivity for L- over D-lactate, and in their sensitivity to inhibitors. There are Na⁺-monocarboxylate cotransporters on the luminal surface of intestinal and kidney epithelia, which allow the uptake of lactate, pyruvate, and ketone bodies in these tissues. In addition, there are specific and selective transporters for organic cations and organic anions

in organs including the kidney, intestine and liver. Organic anion transporters are selective for hydrophobic, charged molecules with electron-attracting side groups. Organic cation transporters, such as the ammonium transporter, mediate the secretion of a variety of drugs and endogenous metabolites, and contribute to the maintenance of intercellular pH (Poole, R.C. and A.P. Halestrap (1993) *Am. J. Physiol.* 264:C761-C782; Price, N.T. et al. (1998) *Biochem. J.* 329:321-328; and Martinelle, K. and I. Haggstrom (1993) *J. Biotechnol.* 30:339-350).

ATP-binding cassette (ABC) transporters are members of a superfamily of membrane proteins that transport substances ranging from small molecules such as ions, sugars, amino acids, peptides, and phospholipids, to lipopeptides, large proteins, and complex hydrophobic drugs. ABC transporters consist of four modules: two nucleotide-binding domains (NBD), which hydrolyze ATP to supply the energy required for transport, and two membrane-spanning domains (MSD), each containing six putative transmembrane segments. These four modules may be encoded by a single gene, as is the case for the cystic fibrosis transmembrane regulator (CFTR), or by separate genes. When encoded by separate genes, each gene product contains a single NBD and MSD. These "half-molecules" form homo- and heterodimers, such as Tap1 and Tap2, the endoplasmic reticulum-based major histocompatibility (MHC) peptide transport system. Several genetic diseases are attributed to defects in ABC transporters, such as the following diseases and their corresponding proteins: cystic fibrosis (CFTR, an ion channel), adrenoleukodystrophy (adrenoleukodystrophy protein, ALDP), Zellweger syndrome (peroxisomal membrane protein-70, PMP70), and hyperinsulinemic hypoglycemia (sulfonylurea receptor, SUR). Overexpression of the multidrug resistance (MDR) protein, another ABC transporter, in human cancer cells makes the cells resistant to a variety of cytotoxic drugs used in chemotherapy (Taglicht, D. and S. Michaelis (1998) *Meth. Enzymol.* 292:130-162).

A number of metal ions such as iron, zinc, copper, cobalt, manganese, molybdenum, selenium, nickel, and chromium are important as cofactors for a number of enzymes. For example, copper is involved in hemoglobin synthesis, connective tissue metabolism, and bone development, by acting as a cofactor in oxidoreductases such as superoxide dismutase, ferroxidase (ceruloplasmin), and lysyl oxidase. Copper and other metal ions must be provided in the diet, and are absorbed by transporters in the gastrointestinal tract. Plasma proteins transport the metal ions to the liver and other target organs, where specific transporters move the ions into cells and cellular organelles as needed. Imbalances in metal ion metabolism have been associated with a number of disease states (Danks, D.M. (1986) *J. Med. Genet.* 23:99-106).

Transport of fatty acids across the plasma membrane can occur by diffusion, a high capacity, low affinity process. However, under normal physiological conditions a significant fraction of fatty acid transport appears to occur via a high affinity, low capacity protein-mediated transport process.

Fatty acid transport protein (FATP), an integral membrane protein with four transmembrane segments, is expressed in tissues exhibiting high levels of plasma membrane fatty acid flux, such as muscle, heart, and adipose. Expression of FATP is upregulated in 3T3-L1 cells during adipose conversion, and expression in COS7 fibroblasts elevates uptake of long-chain fatty acids (Hui, T.Y. et al. (1998) J.

5 Biol. Chem. 273:27420-27429).

Mitochondrial carrier proteins are transmembrane-spanning proteins which transport ions and charged metabolites between the cytosol and the mitochondrial matrix. Examples include the ADP, ATP carrier protein; the 2-oxoglutarate/malate carrier; the phosphate carrier protein; the pyruvate carrier; the dicarboxylate carrier which transports malate, succinate, fumarate, and phosphate; the
10 tricarboxylate carrier which transports citrate and malate; and the Grave's disease carrier protein, a protein recognized by IgG in patients with active Grave's disease, an autoimmune disorder resulting in hyperthyroidism. Proteins in this family consist of three tandem repeats of an approximately 100 amino acid domain, each of which contains two transmembrane regions (Stryer, L. (1995) Biochemistry, W.H. Freeman and Company, New York NY, p. 551; PROSITE PDOC00189 Mitochondrial energy transfer
15 proteins signature; Online Mendelian Inheritance in Man (OMIM) *275000 Graves Disease).

This class of transporters also includes the mitochondrial uncoupling proteins, which create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from ATP synthesis. The result is energy dissipation in the form of heat. Mitochondrial uncoupling proteins have been implicated as modulators of thermoregulation and metabolic rate, and have been proposed as
20 potential targets for drugs against metabolic diseases such as obesity (Ricquier, D. et al. (1999) J. Int. Med. 245:637-642).

Ion Channels

The electrical potential of a cell is generated and maintained by controlling the movement of ions across the plasma membrane. The movement of ions requires ion channels, which form ion-
25 selective pores within the membrane. There are two basic types of ion channels, ion transporters and gated ion channels. Ion transporters utilize the energy obtained from ATP hydrolysis to actively transport an ion against the ion's concentration gradient. Gated ion channels allow passive flow of an ion down the ion's electrochemical gradient under restricted conditions. Together, these types of ion channels generate, maintain, and utilize an electrochemical gradient that is used in 1) electrical impulse
30 conduction down the axon of a nerve cell, 2) transport of molecules into cells against concentration gradients, 3) initiation of muscle contraction, and 4) endocrine cell secretion.

Ion Transporters

Ion transporters generate and maintain the resting electrical potential of a cell. Utilizing the energy derived from ATP hydrolysis, they transport ions against the ion's concentration gradient.

These transmembrane ATPases are divided into three families. The phosphorylated (P) class ion transporters, including Na⁺-K⁺ ATPase, Ca²⁺-ATPase, and H⁺-ATPase, are activated by a phosphorylation event. P-class ion transporters are responsible for maintaining resting potential distributions such that cytosolic concentrations of Na⁺ and Ca²⁺ are low and cytosolic concentration of K⁺ is high. The vacuolar (V) class of ion transporters includes H⁺ pumps on intracellular organelles, such as lysosomes and Golgi. V-class ion transporters are responsible for generating the low pH within the lumen of these organelles that is required for function. The coupling factor (F) class consists of H⁺ pumps in the mitochondria. F-class ion transporters utilize a proton gradient to generate ATP from ADP and inorganic phosphate (P_i).

10 The P-ATPases are hexamers of a 100 kD subunit with ten transmembrane domains and several large cytoplasmic regions that may play a role in ion binding (Scarborough, G.A. (1999) Curr. Opin. Cell Biol. 11:517-522). The V-ATPases are composed of two functional domains: the V₁ domain, a peripheral complex responsible for ATP hydrolysis; and the V₀ domain, an integral complex responsible for proton translocation across the membrane. The F-ATPases are structurally and evolutionarily related to the V-ATPases. The F-ATPase F₀ domain contains 12 copies of the c subunit, a highly hydrophobic protein composed of two transmembrane domains and containing a single buried carboxyl group in TM2 that is essential for proton transport. The V-ATPase V₀ domain contains three types of homologous c subunits with four or five transmembrane domains and the essential carboxyl group in TM4 or TM3. Both types of complex also contain a single a subunit that
15
20 may be involved in regulating the pH dependence of activity (Forgac, M. (1999) J. Biol. Chem. 274:12951-12954).

The resting potential of the cell is utilized in many processes involving carrier proteins and gated ion channels. Carrier proteins utilize the resting potential to transport molecules into and out of the cell. Amino acid and glucose transport into many cells is linked to sodium ion co-transport (symport) so that the movement of Na⁺ down an electrochemical gradient drives transport of the other molecule up a concentration gradient. Similarly, cardiac muscle links transfer of Ca²⁺ out of the cell with transport of Na⁺ into the cell (antiport).

Gated Ion Channels

Gated ion channels control ion flow by regulating the opening and closing of pores. The ability to control ion flux through various gating mechanisms allows ion channels to mediate such diverse signaling and homeostatic functions as neuronal and endocrine signaling, muscle contraction, fertilization, and regulation of ion and pH balance. Gated ion channels are categorized according to the manner of regulating the gating function. Mechanically-gated channels open their pores in response to mechanical stress; voltage-gated channels (e.g., Na⁺, K⁺, Ca²⁺, and Cl⁻ channels) open
30
35 their pores in response to changes in membrane potential; and ligand-gated channels (e.g.,

acetylcholine-, serotonin-, and glutamate-gated cation channels, and GABA- and glycine-gated chloride channels) open their pores in the presence of a specific ion, nucleotide, or neurotransmitter. The gating properties of a particular ion channel (i.e., its threshold for and duration of opening and closing) are sometimes modulated by association with auxiliary channel proteins and/or post

5 translational modifications, such as phosphorylation.

Mechanically-gated or mechanosensitive ion channels act as transducers for the senses of touch, hearing, and balance, and also play important roles in cell volume regulation, smooth muscle contraction, and cardiac rhythm generation. A stretch-inactivated channel (SIC) was recently cloned from rat kidney. The SIC channel belongs to a group of channels which are activated by pressure or

10 stress on the cell membrane and conduct both Ca^{2+} and Na^{+} (Suzuki, M. et al. (1999) J. Biol. Chem. 274:6330-6335).

The pore-forming subunits of the voltage-gated cation channels form a superfamily of ion channel proteins. The characteristic domain of these channel proteins comprises six transmembrane domains (S1-S6), a pore-forming region (P) located between S5 and S6, and intracellular amino and

15 carboxy termini. In the Na^{+} and Ca^{2+} subfamilies, this domain is repeated four times, while in the K^{+} channel subfamily, each channel is formed from a tetramer of either identical or dissimilar subunits. The P region contains information specifying the ion selectivity for the channel. In the case of K^{+} channels, a GYG tripeptide is involved in this selectivity (Ishii, T.M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11651-11656).

20 Voltage-gated Na^{+} and K^{+} channels are necessary for the function of electrically excitable cells, such as nerve and muscle cells. Action potentials, which lead to neurotransmitter release and muscle contraction, arise from large, transient changes in the permeability of the membrane to Na^{+} and K^{+} ions. Depolarization of the membrane beyond the threshold level opens voltage-gated Na^{+} channels. Sodium ions flow into the cell, further depolarizing the membrane and opening more voltage-gated Na^{+}

25 channels, which propagates the depolarization down the length of the cell. Depolarization also opens voltage-gated potassium channels. Consequently, potassium ions flow outward, which leads to repolarization of the membrane. Voltage-gated channels utilize charged residues in the fourth transmembrane segment (S4) to sense voltage change. The open state lasts only about 1 millisecond, at which time the channel spontaneously converts into an inactive state that cannot be opened irrespective

30 of the membrane potential. Inactivation is mediated by the channel's N-terminus, which acts as a plug that closes the pore. The transition from an inactive to a closed state requires a return to resting potential.

Voltage-gated Na^{+} channels are heterotrimeric complexes composed of a 260 kDa pore-forming α subunit that associates with two smaller auxiliary subunits, $\beta 1$ and $\beta 2$. The $\beta 2$ subunit is a integral

membrane glycoprotein that contains an extracellular Ig domain, and its association with α and $\beta 1$ subunits correlates with increased functional expression of the channel, a change in its gating properties, as well as an increase in whole cell capacitance due to an increase in membrane surface area (Isom, L.L. et al. (1995) Cell 83:433-442).

- 5 Non voltage-gated Na^+ channels include the members of the amiloride-sensitive Na^+ channel/degenerin (NaC/DEG) family. Channel subunits of this family are thought to consist of two transmembrane domains flanking a long extracellular loop, with the amino and carboxyl termini located within the cell. The NaC/DEG family includes the epithelial Na^+ channel (ENaC) involved in Na^+ reabsorption in epithelia including the airway, distal colon, cortical collecting duct of the kidney, and
- 10 exocrine duct glands. Mutations in ENaC result in pseudohypoaldosteronism type 1 and Liddle's syndrome (pseudohyperaldosteronism). The NaC/DEG family also includes the recently characterized H^+ -gated cation channels or acid-sensing ion channels (ASIC). ASIC subunits are expressed in the brain and form heteromultimeric Na^+ -permeable channels. These channels require acid pH fluctuations for activation. ASIC subunits show homology to the degenerins, a family of mechanically-gated
- 15 channels originally isolated from *C. elegans*. Mutations in the degenerins cause neurodegeneration. ASIC subunits may also have a role in neuronal function, or in pain perception, since tissue acidosis causes pain (Waldmann, R. and M. Lazdunski (1998) Curr. Opin. Neurobiol. 8:418-424; Eglén, R.M. et al. (1999) Trends Pharmacol. Sci. 20:337-342).

- K^+ channels are located in all cell types, and may be regulated by voltage, ATP concentration,
- 20 or second messengers such as Ca^{2+} and cAMP. In non-excitabile tissue, K^+ channels are involved in protein synthesis, control of endocrine secretions, and the maintenance of osmotic equilibrium across membranes. In neurons and other excitable cells, in addition to regulating action potentials and repolarizing membranes, K^+ channels are responsible for setting resting membrane potential. The cytosol contains non-diffusible anions and, to balance this net negative charge, the cell contains a Na^+ -
- 25 K^+ pump and ion channels that provide the redistribution of Na^+ , K^+ , and Cl^- . The pump actively transports Na^+ out of the cell and K^+ into the cell in a 3:2 ratio. Ion channels in the plasma membrane allow K^+ and Cl^- to flow by passive diffusion. Because of the high negative charge within the cytosol, Cl^- flows out of the cell. The flow of K^+ is balanced by an electromotive force pulling K^+ into the cell, and a K^+ concentration gradient pushing K^+ out of the cell. Thus, the resting membrane potential is
- 30 primarily regulated by K^+ flow (Salkoff, L. and T. Jegla (1995) Neuron 15:489-492).

Potassium channel subunits of the Shaker-like superfamily all have the characteristic six transmembrane/1 pore domain structure. Four subunits combine as homo- or heterotetramers to form functional K channels. These pore-forming subunits also associate with various cytoplasmic β subunits that alter channel inactivation kinetics. The Shaker-like channel family includes the voltage-

gated K⁺ channels as well as the delayed rectifier type channels such as the human ether-a-go-go related gene (HERG) associated with long QT, a cardiac dysrhythmia syndrome (Curran, M.E. (1998) *Curr. Opin. Biotechnol.* 9:565-572; Kaczorowski, G.J. and M.L. Garcia (1999) *Curr. Opin. Chem. Biol.* 3:448-458).

- 5 A second superfamily of K⁺ channels is composed of the inward rectifying channels (Kir). Kir channels have the property of preferentially conducting K⁺ currents in the inward direction. These proteins consist of a single potassium selective pore domain and two transmembrane domains, which correspond to the fifth and sixth transmembrane domains of voltage-gated K⁺ channels. Kir subunits also associate as tetramers. The Kir family includes ROMK1, mutations in which lead to Bartter
- 10 syndrome, a renal tubular disorder. Kir channels are also involved in regulation of cardiac pacemaker activity, seizures and epilepsy, and insulin regulation (Doupnik, C.A. et al. (1995) *Curr. Opin. Neurobiol.* 5:268-277; Curran, *supra*).

- The recently recognized TWIK K⁺ channel family includes the mammalian TWIK-1, TREK-1 and TASK proteins. Members of this family possess an overall structure with four transmembrane
- 15 domains and two P domains. These proteins are probably involved in controlling the resting potential in a large set of cell types (Duprat, F. et al. (1997) *EMBO J* 16:5464-5471).

- The voltage-gated Ca²⁺ channels have been classified into several subtypes based upon their electrophysiological and pharmacological characteristics. L-type Ca²⁺ channels are predominantly expressed in heart and skeletal muscle where they play an essential role in excitation-contraction
- 20 coupling. T-type channels are important for cardiac pacemaker activity, while N-type and P/Q-type channels are involved in the control of neurotransmitter release in the central and peripheral nervous system. The L-type and N-type voltage-gated Ca²⁺ channels have been purified and, though their functions differ dramatically, they have similar subunit compositions. The channels are composed of three subunits. The α_1 subunit forms the membrane pore and voltage sensor, while the $\alpha_2\delta$ and β
- 25 subunits modulate the voltage-dependence, gating properties, and the current amplitude of the channel. These subunits are encoded by at least six α_1 , one $\alpha_2\delta$, and four β genes. A fourth subunit, γ , has been identified in skeletal muscle (Walker, D. et al. (1998) *J. Biol. Chem.* 273:2361-2367; McCleskey, E.W. (1994) *Curr. Opin. Neurobiol.* 4:304-312).

- The transient receptor family (Trp) of calcium ion channels are thought to mediate capacitative
- 30 calcium entry (CCE). CCE is the Ca²⁺ influx into cells to resupply Ca²⁺ stores depleted by the action of inositol triphosphate (IP3) and other agents in response to numerous hormones and growth factors. Trp and Trp-like were first cloned from *Drosophila* and have similarity to voltage gated Ca²⁺ channels in the S3 through S6 regions. This suggests that Trp and/or related proteins may form mammalian CCC entry channels (Zhu, X. et al. (1996) *Cell* 85:661-671; Boulay, G. et al. (1997) *J. Biol. Chem.*

272:29672-29680). Melastatin is a gene isolated in both the mouse and human, and whose expression in melanoma cells is inversely correlated with melanoma aggressiveness in vivo. The human cDNA transcript corresponds to a 1533-amino acid protein having homology to members of the Trp family. It has been proposed that the combined use of malastatin mRNA expression status and tumor thickness
5 might allow for the determination of subgroups of patients at both low and high risk for developing metastatic disease (Duncan, L.M. et al (2001) J. Clin. Oncol. 19:568-576).

Chloride channels are necessary in endocrine secretion and in regulation of cytosolic and organelle pH. In secretory epithelial cells, Cl^- enters the cell across a basolateral membrane through an Na^+ , K^+/Cl^- cotransporter, accumulating in the cell above its electrochemical equilibrium concentration.
10 Secretion of Cl^- from the apical surface, in response to hormonal stimulation, leads to flow of Na^+ and water into the secretory lumen. The cystic fibrosis transmembrane conductance regulator (CFTR) is a chloride channel encoded by the gene for cystic fibrosis, a common fatal genetic disorder in humans. CFTR is a member of the ABC transporter family, and is composed of two domains each consisting of six transmembrane domains followed by a nucleotide-binding site. Loss of CFTR function decreases
15 transepithelial water secretion and, as a result, the layers of mucus that coat the respiratory tree, pancreatic ducts, and intestine are dehydrated and difficult to clear. The resulting blockage of these sites leads to pancreatic insufficiency, "meconium ileus", and devastating "chronic obstructive pulmonary disease" (Al-Awqati, Q. et al. (1992) J. Exp. Biol. 172:245-266).

The voltage-gated chloride channels (CLC) are characterized by 10-12 transmembrane
20 domains, as well as two small globular domains known as CBS domains. The CLC subunits probably function as homotetramers. CLC proteins are involved in regulation of cell volume, membrane potential stabilization, signal transduction, and transepithelial transport. Mutations in CLC-1, expressed predominantly in skeletal muscle, are responsible for autosomal recessive generalized myotonia and autosomal dominant myotonia congenita, while mutations in the kidney channel CLC-5
25 lead to kidney stones (Jentsch, T.J. (1996) Curr. Opin. Neurobiol. 6:303-310).

Ligand-gated channels open their pores when an extracellular or intracellular mediator binds to the channel. Neurotransmitter-gated channels are channels that open when a neurotransmitter binds to their extracellular domain. These channels exist in the postsynaptic membrane of nerve or muscle cells. There are two types of neurotransmitter-gated channels. Sodium channels open in response to
30 excitatory neurotransmitters, such as acetylcholine, glutamate, and serotonin. This opening causes an influx of Na^+ and produces the initial localized depolarization that activates the voltage-gated channels and starts the action potential. Chloride channels open in response to inhibitory neurotransmitters, such as γ -aminobutyric acid (GABA) and glycine, leading to hyperpolarization of the membrane and the subsequent generation of an action potential. Neurotransmitter-gated ion channels have four

transmembrane domains and probably function as pentamers (Jentsch, supra). Amino acids in the second transmembrane domain appear to be important in determining channel permeation and selectivity (Sather, W.A. et al. (1994) *Curr. Opin. Neurobiol.* 4:313-323).

Ligand-gated channels can be regulated by intracellular second messengers. For example, calcium-activated K^+ channels are gated by internal calcium ions. In nerve cells, an influx of calcium during depolarization opens K^+ channels to modulate the magnitude of the action potential (Ishi et al., supra). The large conductance (BK) channel has been purified from brain and its subunit composition determined. The α subunit of the BK channel has seven rather than six transmembrane domains in contrast to voltage-gated K^+ channels. The extra transmembrane domain is located at the subunit N-terminus. A 28-amino-acid stretch in the C-terminal region of the subunit (the "calcium bowl" region) contains many negatively charged residues and is thought to be the region responsible for calcium binding. The β subunit consists of two transmembrane domains connected by a glycosylated extracellular loop, with intracellular N- and C-termini (Kaczorowski, supra; Vergara, C. et al. (1998) *Curr. Opin. Neurobiol.* 8:321-329).

Cyclic nucleotide-gated (CNG) channels are gated by cytosolic cyclic nucleotides. The best examples of these are the cAMP-gated Na^+ channels involved in olfaction and the cGMP-gated cation channels involved in vision. Both systems involve ligand-mediated activation of a G-protein coupled receptor which then alters the level of cyclic nucleotide within the cell. CNG channels also represent a major pathway for Ca^{2+} entry into neurons, and play roles in neuronal development and plasticity. CNG channels are tetramers containing at least two types of subunits, an α subunit which can form functional homomeric channels, and a β subunit, which modulates the channel properties. All CNG subunits have six transmembrane domains and a pore forming region between the fifth and sixth transmembrane domains, similar to voltage-gated K^+ channels. A large C-terminal domain contains a cyclic nucleotide binding domain, while the N-terminal domain confers variation among channel subtypes (Zufall, F. et al. (1997) *Curr. Opin. Neurobiol.* 7:404-412).

The activity of other types of ion channel proteins may also be modulated by a variety of intracellular signalling proteins. Many channels have sites for phosphorylation by one or more protein kinases including protein kinase A, protein kinase C, tyrosine kinase, and casein kinase II, all of which regulate ion channel activity in cells. Kir channels are activated by the binding of the $G\beta\gamma$ subunits of heterotrimeric G-proteins (Reimann, F. and F.M. Ashcroft (1999) *Curr. Opin. Cell. Biol.* 11:503-508). Other proteins are involved in the localization of ion channels to specific sites in the cell membrane. Such proteins include the PDZ domain proteins known as MAGUKs (membrane-associated guanylate kinases) which regulate the clustering of ion channels at neuronal synapses (Craven, S.E. and D.S. Bredt (1998) *Cell* 93:495-498).

Disease Correlation

The etiology of numerous human diseases and disorders can be attributed to defects in the transport of molecules across membranes. Defects in the trafficking of membrane-bound transporters and ion channels are associated with several disorders, e.g., cystic fibrosis, glucose-galactose
 5 malabsorption syndrome, hypercholesterolemia, von Gierke disease, and certain forms of diabetes mellitus. Single-gene defect diseases resulting in an inability to transport small molecules across membranes include, e.g., cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease (van't Hoff, W.G. (1996) *Exp. Nephrol.* 4:253-262; Talente, G.M. et al. (1994) *Ann. Intern. Med.* 120:218-226; and Chillon, M. et al. (1995) *New Engl. J. Med.* 332:1475-1480).

10 Human diseases caused by mutations in ion channel genes include disorders of skeletal muscle, cardiac muscle, and the central nervous system. Mutations in the pore-forming subunits of sodium and chloride channels cause myotonia, a muscle disorder in which relaxation after voluntary contraction is delayed. Sodium channel myotonias have been treated with channel blockers. Mutations in muscle sodium and calcium channels cause forms of periodic paralysis, while mutations in the sarcoplasmic
 15 calcium release channel, T-tubule calcium channel, and muscle sodium channel cause malignant hyperthermia. Cardiac arrhythmia disorders such as the long QT syndromes and idiopathic ventricular fibrillation are caused by mutations in potassium and sodium channels (Cooper, E.C. and L.Y. Jan (1998) *Proc. Natl. Acad. Sci. USA* 96:4759-4766). All four known human idiopathic epilepsy genes code for ion channel proteins (Berkovic, S.F. and I.E. Scheffer (1999) *Curr. Opin. Neurology* 12:177-
 20 182). Other neurological disorders such as ataxias, hemiplegic migraine and hereditary deafness can also result from mutations in ion channel genes (Jen, J. (1999) *Curr. Opin. Neurobiol.* 9:274-280; Cooper, *supra*).

Ion channels have been the target for many drug therapies. Neurotransmitter-gated channels have been targeted in therapies for treatment of insomnia, anxiety, depression, and schizophrenia.
 25 Voltage-gated channels have been targeted in therapies for arrhythmia, ischemic stroke, head trauma, and neurodegenerative disease (Taylor, C.P. and L.S. Narasimhan (1997) *Adv. Pharmacol.* 39:47-98). Various classes of ion channels also play an important role in the perception of pain, and thus are potential targets for new analgesics. These include the vanilloid-gated ion channels, which are activated by the vanilloid capsaicin, as well as by noxious heat. Local anesthetics such as lidocaine and
 30 mexiletine which blockade voltage-gated Na⁺ channels have been useful in the treatment of neuropathic pain (Eglen, *supra*).

Ion channels in the immune system have recently been suggested as targets for immunomodulation. T-cell activation depends upon calcium signaling, and a diverse set of T-cell specific ion channels has been characterized that affect this signaling process. Channel blocking agents

can inhibit secretion of lymphokines, cell proliferation, and killing of target cells. A peptide antagonist of the T-cell potassium channel Kv1.3 was found to suppress delayed-type hypersensitivity and allogenic responses in pigs, validating the idea of channel blockers as safe and efficacious immunosuppressants (Cahalan, M.D. and K.G. Chandy (1997) Curr. Opin. Biotechnol. 8:749-756).

The discovery of new transporters and ion channels, and the polynucleotides encoding them, satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of transport, neurological, muscle, immunological, and cell proliferative disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, transporters and ion channels, referred to collectively as "TRICH" and individually as "TRICH-1," "TRICH-2," "TRICH-3," "TRICH-4," "TRICH-5," "TRICH-6," "TRICH-7," "TRICH-8," "TRICH-9," "TRICH-10," "TRICH-11," "TRICH-12," "TRICH-13," "TRICH-14," "TRICH-15," "TRICH-16," "TRICH-17," "TRICH-18," "TRICH-19," "TRICH-20," "TRICH-21," "TRICH-22," "TRICH-23," "TRICH-24," "TRICH-25," "TRICH-26," "TRICH-27," "TRICH-28," "TRICH-29," "TRICH-30," "TRICH-31," and "TRICH-32." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-32.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-32. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:33-64.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32.

The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional TRICH, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. The method comprises a) combining the polypeptide with at least one test compound under

suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:33-64, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the

polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the present invention.

Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of the polypeptides.

Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide sequences of the invention, along with selected fragments of the polynucleotide sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a

reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although
5 any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is
10 not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

“TRICH” refers to the amino acid sequences of substantially purified TRICH obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

15 The term “agonist” refers to a molecule which intensifies or mimics the biological activity of TRICH. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TRICH either by directly interacting with TRICH or by acting on components of the biological pathway in which TRICH participates.

An “allelic variant” is an alternative form of the gene encoding TRICH. Allelic variants may
20 result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in
25 a given sequence.

“Altered” nucleic acid sequences encoding TRICH include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as TRICH or a polypeptide with at least one functional characteristic of TRICH. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of
30 the polynucleotide encoding TRICH, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding TRICH. The encoded protein may also be “altered,” and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent TRICH. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge,

solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of TRICH is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of TRICH. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TRICH either by directly interacting with TRICH or by acting on components of the biological pathway in which TRICH participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind TRICH polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic TRICH, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding TRICH or fragments of TRICH may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

“Conservative amino acid substitutions” are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as

5 conservative amino acid substitutions.

	Original Residue	Conservative Substitution
	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
10	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
15	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
20	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
25	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the
30 side chain.

A “deletion” refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term “derivative” refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one
35 biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A “detectable label” refers to a reporter molecule or enzyme that is capable of generating a
40 measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

“Differential expression” refers to increased or upregulated; or decreased, downregulated, or

absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

A "fragment" is a unique portion of TRICH or the polynucleotide encoding TRICH which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:33-64 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:33-64, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:33-64 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:33-64 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:33-64 and the region of SEQ ID NO:33-64 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-32 is encoded by a fragment of SEQ ID NO:33-64. A fragment of SEQ ID NO:1-32 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-32. For example, a fragment of SEQ ID NO:1-32 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-32. The precise length of a fragment of SEQ ID NO:1-32 and the region of SEQ ID NO:1-32 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to

the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore, achieve a more meaningful comparison of the two sequences.

- 5 Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191.
- 10 For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

- Alternatively, a suite of commonly used and freely available sequence comparison algorithms is
- 15 provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other
- 20 polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to
- 25 compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

- 30 *Open Gap: 5 and Extension Gap: 2 penalties*

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for

example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term “humanized antibody” refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour.

Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

10 The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells
15 or their nucleic acids have been fixed).

 The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

 "Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of
20 various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

 An "immunogenic fragment" is a polypeptide or oligopeptide fragment of TRICH which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of
25 TRICH which is useful in any of the antibody production methods disclosed herein or known in the art.

 The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

 The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

30 The term "modulate" refers to a change in the activity of TRICH. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of TRICH.

 The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or

synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably
5 linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of
10 amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

"Post-translational modification" of an TRICH may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the
15 art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of TRICH.

"Probe" refers to nucleic acid sequences encoding TRICH, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical
20 labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

25 Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the
30 specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR

Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

5 Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU
10 primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer
15 binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that
20 hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary
25 polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the
30 artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

5 A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent,
10 chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose
15 instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing TRICH, nucleic acids encoding TRICH, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

20 The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding-molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope
25 A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which
30 they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers,

microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

5 "Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection,
10 electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "transgenic organism," as used herein, is any organism, including but not limited to
15 animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in
20 vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention
25 into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999)
30 set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant

identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule.

Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

The invention is based on the discovery of new human transporters and ion channels (TRICH), the polynucleotides encoding TRICH, and the use of these compositions for the diagnosis, treatment, or prevention of transport, neurological, muscle, immunological, and cell proliferative disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank

homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are transporters and ion channels. For example, SEQ ID NO:5 is 83% identical to rat GABA receptor rho-3 subunit precursor (GenBank ID g1060975) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.7e-206$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:5 also contains a neurotransmitter-gated ion channel domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:5 is a neurotransmitter-gated ion channel. In an alternate example, SEQ ID NO:16 is 57% identical to human Na⁺/glucose cotransporter (GenBank ID g338055) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $2.4e-181$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:16 also contains a sodium:solute symporter family domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:16 is a Na⁺/glucose cotransporter. In an alternate example, SEQ ID NO:27 is 53% identical to human ATP-binding cassette transporter-1 (ABC-1) (GenBank ID g4128033) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:27 also contains an ABC transporter domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from

BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:27 is an ABC transporter. In an alternate example, SEQ ID NO:12 is 45% identical to rat thyroid sodium/iodide symporter NIS (GenBank ID g1399954) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $3.0e-143$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:12 also contains a sodium:solute symporter family domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:12 is a sodium:solute symporter. SEQ ID NO:1-4, SEQ ID NO:6-11, SEQ ID NO:13-15, SEQ ID NO:17-26, and SEQ ID NO:28-32 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-32 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:33-64 or that distinguish between SEQ ID NO:33-64 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 6724643H1 is the identification number of an Incyte cDNA sequence, and LUNLTMT01 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 71495515V1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs (e.g., g5746200) which contributed to the assembly of the full length polynucleotide sequences. In addition, the identification numbers in column 5 may identify sequences derived from the ENSEMBL (The Sanger Centre, Cambridge, UK) database (*i.e.*, those sequences

- including the designation "ENST"). Alternatively, the identification numbers in column 5 may be derived from the NCBI RefSeq Nucleotide Sequence Records Database (*i.e.*, those sequences including the designation "NM" or "NT") or the NCBI RefSeq Protein Sequence Records (*i.e.*, those sequences including the designation "NP"). Alternatively, the identification numbers in column 5 may refer to
- 5 assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. For example, FL_XXXXXX_N₁_N₂YYYY_N₃_N₄ represents a "stitched" sequence in which XXXXXX is the identification number of the cluster of sequences to which the algorithm was applied, and YYYY is the number of the prediction generated by the algorithm, and N_{1,2,3...}, if present, represent specific exons that may have been manually edited during analysis (See Example V).
- 10 Alternatively, the identification numbers in column 5 may refer to assemblages of exons brought together by an "exon-stretching" algorithm. For example, FLXXXXXX_gAAAAA_gBBBBB_1_N is the identification number of a "stretched" sequence, with XXXXXX being the Incyte project identification number, gAAAAA being the GenBank identification number of the human genomic sequence to which the "exon-stretching" algorithm was applied, gBBBBB being the GenBank identification number or
- 15 NCBI RefSeq identification number of the nearest GenBank protein homolog, and N referring to specific exons (See Example V). In instances where a RefSeq sequence was used as a protein homolog for the "exon-stretching" algorithm, a RefSeq identifier (denoted by "NM," "NP," or "NT") may be used in place of the GenBank identifier (*i.e.*, gBBBBB).

- Alternatively, a prefix identifies component sequences that were hand-edited, predicted from
- 20 genomic DNA sequences, or derived from a combination of sequence analysis methods. The following Table lists examples of component sequence prefixes and corresponding sequence analysis methods associated with the prefixes (see Example IV and Example V).

Prefix	Type of analysis and/or examples of programs
GNN, GFG, ENST	Exon prediction from genomic sequences using, for example, GENSCAN (Stanford University, CA, USA) or FGENES (Computer Genomics Group, The Sanger Centre, Cambridge, UK).
GBI	Hand-edited analysis of genomic sequences.
FL	Stitched or stretched genomic sequences (see Example V).

- In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column
- 30 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte

cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

The invention also encompasses TRICH variants. A preferred TRICH variant is one which has
5 at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the TRICH amino acid sequence, and which contains at least one functional or structural characteristic of TRICH.

The invention also encompasses polynucleotides which encode TRICH. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from
10 the group consisting of SEQ ID NO:33-64, which encodes TRICH. The polynucleotide sequences of SEQ ID NO:33-64, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding TRICH. In
15 particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding TRICH. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:33-64 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide
20 sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:33-64. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of TRICH.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding TRICH, some bearing minimal similarity to the
25 polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring TRICH, and all such variations are to be considered as being specifically disclosed.

30 Although nucleotide sequences which encode TRICH and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring TRICH under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding TRICH or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide

occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding TRICH and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode TRICH and TRICH derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding TRICH or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:33-64 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding TRICH may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic

DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode TRICH may be cloned in recombinant DNA molecules that direct expression of TRICH, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of

the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express TRICH.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter TRICH-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of TRICH, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding TRICH may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.) Alternatively, TRICH itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of TRICH, or any part thereof, may be altered during direct synthesis and/or combined with sequences

from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.)

- 5 The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, *supra*, pp. 28-53.)

In order to express a biologically active TRICH, the nucleotide sequences encoding TRICH or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a
10 suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding TRICH. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding TRICH. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where
15 sequences encoding TRICH and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural
20 and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding TRICH and appropriate transcriptional and translational control
25 elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences
30 encoding TRICH. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or

animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al. (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding TRICH. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding TRICH can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSFORT1 plasmid (Life Technologies). Ligation of sequences encoding TRICH into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of TRICH are needed, e.g. for the production of antibodies, vectors which direct high level expression of TRICH may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of TRICH. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; and Scorer, C.A. et al. (1994) Bio/Technology 12:181-184.)

Plant systems may also be used for expression of TRICH. Transcription of sequences encoding TRICH may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311).

Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, 5 e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding TRICH may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader 10 sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses TRICH in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

15 Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of 20 TRICH in cell lines is preferred. For example, sequences encoding TRICH can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a 25 selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase 30 genes, for use in *tk⁻* and *apr⁻* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980)

Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding TRICH is inserted within a marker gene sequence, transformed cells containing sequences encoding TRICH can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding TRICH under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding TRICH and that express TRICH may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of TRICH using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on TRICH is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding TRICH include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding TRICH, or any fragments thereof, may be cloned into a vector for

the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega
5 (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding TRICH may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein
10 produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode TRICH may be designed to contain signal sequences which direct secretion of TRICH through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the
15 inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities
20 (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding TRICH may be ligated to a heterologous sequence resulting in translation of a
25 fusion protein in any of the aforementioned host systems. For example, a chimeric TRICH protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of TRICH activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose
30 binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize

these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the TRICH encoding sequence and the heterologous protein sequence, so that TRICH may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially
5 available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled TRICH may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for
10 example, ³⁵S-methionine.

TRICH of the present invention or fragments thereof may be used to screen for compounds that specifically bind to TRICH. At least one and up to a plurality of test compounds may be screened for specific binding to TRICH. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

15 In one embodiment, the compound thus identified is closely related to the natural ligand of TRICH, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which TRICH binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the
20 compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express TRICH, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing TRICH or cell membrane fractions which contain TRICH are then contacted with a test compound and binding, stimulation, or inhibition of activity of either TRICH or the
25 compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with TRICH, either in solution or affixed to a solid support, and detecting the binding of TRICH to the compound.
30 Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

TRICH of the present invention or fragments thereof may be used to screen for compounds
35 that modulate the activity of TRICH. Such compounds may include agonists, antagonists, or partial

or inverse agonists. In one embodiment, an assay is performed under conditions permissive for TRICH activity, wherein TRICH is combined with at least one test compound, and the activity of TRICH in the presence of a test compound is compared with the activity of TRICH in the absence of the test compound. A change in the activity of TRICH in the presence of the test compound is indicative of a compound that modulates the activity of TRICH. Alternatively, a test compound is combined with an in vitro or cell-free system comprising TRICH under conditions suitable for TRICH activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of TRICH may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding TRICH or their mammalian homologs may be “knocked out” in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding TRICH may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding TRICH can also be used to create “knockin” humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding TRICH is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with

potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress TRICH, e.g., by secreting TRICH in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) *Biotechnol. Annu. Rev.* 4:55-74).

THERAPEUTICS

5 Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of TRICH and transporters and ion channels. In addition, the expression of TRICH is closely associated with adrenal, testicular, and prostate tumors, Crohn's disease, teratocarcinoma and dendritic cells, brain, lung, ileum, small intestine, uterine myometrial, colon, and pancreatic tissues. Therefore, TRICH appears to play a role in transport, neurological, muscle, immunological,
10 and cell proliferative disorders. In the treatment of disorders associated with increased TRICH expression or activity, it is desirable to decrease the expression or activity of TRICH. In the treatment of disorders associated with decreased TRICH expression or activity, it is desirable to increase the expression or activity of TRICH.

 Therefore, in one embodiment, TRICH or a fragment or derivative thereof may be
15 administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH. Examples of such disorders include, but are not limited to, a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic
20 periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy,
25 ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery
30 stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms,
35 Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other

extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous

5 system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic

10 nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses,

15 postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy,

20 ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, pheochromocytoma, and myopathies including encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, ophthalmoplegia, and acid maltase deficiency (AMD, also known as Pompe's disease); an immunological disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease,

25 adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic

30 gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative

35 colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal

circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including
5 adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing TRICH or a fragment or derivative
10 thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified TRICH in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those
15 provided above.

In still another embodiment, an agonist which modulates the activity of TRICH may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRICH including, but not limited to, those listed above.

In a further embodiment, an antagonist of TRICH may be administered to a subject to treat or
20 prevent a disorder associated with increased expression or activity of TRICH. Examples of such disorders include, but are not limited to, those transport, neurological, muscle, immunological, and cell proliferative disorders described above. In one aspect, an antibody which specifically binds TRICH may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express TRICH.

25 In an additional embodiment, a vector expressing the complement of the polynucleotide encoding TRICH may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TRICH including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate
30 therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of TRICH may be produced using methods which are generally known in the art. In particular, purified TRICH may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind TRICH. Antibodies to TRICH may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with TRICH or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to TRICH have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of TRICH amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to TRICH may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce TRICH-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be

generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for TRICH may also be generated. For example, such fragments include, but are not limited to, $F(ab')_2$ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between TRICH and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering TRICH epitopes is generally used, but a competitive binding assay may also be employed (Pound, *supra*).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for TRICH. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of TRICH-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple TRICH epitopes, represents the average affinity, or avidity, of the antibodies for TRICH. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular TRICH epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the TRICH-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of TRICH, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of TRICH-antibody
 5 complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding TRICH, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene
 10 expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding TRICH. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding TRICH. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense
 15 sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral
 20 vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding TRICH may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked
 30 inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial

hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and N. Somia (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in TRICH expression or regulation causes disease, the expression of TRICH from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in TRICH are treated by constructing mammalian expression vectors encoding TRICH and introducing these vectors by mechanical means into TRICH-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of TRICH include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). TRICH may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl. Acad. Sci. USA 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding TRICH from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver

polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these
5 standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to TRICH expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding TRICH under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive
10 element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for
15 receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a
20 method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al.
25 (1998) *Proc. Natl. Acad. Sci. USA* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding TRICH to cells which have one or more genetic abnormalities with respect to the expression of TRICH. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be
30 versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) *Transplantation* 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) *Annu.*

Rev. Nutr. 19:511-544 and Verma, I.M. and N. Somia (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding TRICH to target cells which have one or more genetic abnormalities with respect to the expression of TRICH. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing TRICH to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding TRICH to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for TRICH into the alphavirus genome in place of the capsid-coding region results in the production of a large number of TRICH-coding RNAs and the synthesis of high levels of TRICH in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application

(Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of TRICH into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and
5 performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases,
10 transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

15 Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding TRICH.

20 Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of
25 candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis.
30 Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding TRICH. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be
5 extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding TRICH.

10 Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or
15 promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased TRICH expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding TRICH may be therapeutically useful, and in the treatment of disorders associated with decreased TRICH expression or activity, a compound which specifically promotes expression of the polynucleotide encoding TRICH may be therapeutically useful.

20 At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound
25 based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding TRICH is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding TRICH are assayed
30 by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding TRICH. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide
35 exposed to a test compound indicates that the test compound is effective in altering the expression of

the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys.

5 Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruice, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruice, T.W. et al. (2000) U.S. Patent No. 6,022,691).

10 Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

20 An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of TRICH, antibodies to TRICH, and mimetics, agonists, antagonists, or inhibitors of TRICH.

25 The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

30 Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S.

Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of
5 an effective dose is well within the capability of those skilled in the art.

Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising TRICH or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, TRICH or a fragment thereof may be joined to a short cationic N-
10 terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys,
15 or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example TRICH or fragments thereof, antibodies of TRICH, and agonists, antagonists or inhibitors of TRICH, which
20 ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large
25 therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

30 The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy.

Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

10 In another embodiment, antibodies which specifically bind TRICH may be used for the diagnosis of disorders characterized by expression of TRICH, or in assays to monitor patients being treated with TRICH or agonists, antagonists, or inhibitors of TRICH. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for TRICH include methods which utilize the antibody and a label to detect TRICH in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring TRICH, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of TRICH expression. Normal or standard values for TRICH expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to TRICH under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of TRICH expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding TRICH may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of TRICH may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of TRICH, and to monitor regulation of TRICH levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding TRICH or closely related molecules may be used to identify nucleic acid sequences which encode TRICH. The specificity of the probe, whether it is made

from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding TRICH, allelic variants, or related sequences.

- 5 Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the TRICH encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:33-64 or from genomic sequences including promoters, enhancers, and introns of the TRICH gene.

- Means for producing specific hybridization probes for DNAs encoding TRICH include the
 10 cloning of polynucleotide sequences encoding TRICH or TRICH derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels, such as
 15 alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

- Polynucleotide sequences encoding TRICH may be used for the diagnosis of disorders associated with expression of TRICH. Examples of such disorders include, but are not limited to, a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes
 20 insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia, tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis,
 25 cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, polymyositis, neurological disorders associated with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with transport, e.g., neurofibromatosis,
 30 postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolemia, adrenoleukodystrophy, Zellweger syndrome, Menkes disease, occipital horn syndrome, von Gierke disease, cystinuria, iminoglycinuria, Hartup disease, and

Fanconi disease; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple
 5 sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis,
 10 encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental
 15 disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a muscle disorder such as cardiomyopathy, myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core
 20 disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, pheochromocytoma, and myopathies including encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic
 25 disorder, ophthalmoplegia, and acid maltase deficiency (AMD, also known as Pompe's disease); an immunological disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact
 30 dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis,
 35 psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic

anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. The polynucleotide sequences encoding TRICH may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered TRICH expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding TRICH may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding TRICH may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding TRICH in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of TRICH, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding TRICH, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several
5 days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ
10 preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding TRICH may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding
15 TRICH, or a fragment of a polynucleotide complementary to the polynucleotide encoding TRICH, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences
20 encoding TRICH may be used to detect single nucleotide polymorphism (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding TRICH are used to amplify DNA using the
25 polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as
30 DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the

alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of TRICH include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, TRICH, fragments of TRICH, or antibodies specific for TRICH may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention
5 may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000)
10 Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested
15 compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for
20 example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample
25 containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples
30 are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are

analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by
5 isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently
10 positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of
15 at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for TRICH to quantify the levels of TRICH expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the
20 levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoz, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should
25 be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid
30 degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference

in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding TRICH may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, for example, Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding TRICH on a physical

map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps.

- 5 Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences
10 mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

- In another embodiment of the invention, TRICH, its catalytic or immunogenic fragments, or
15 oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between TRICH and the agent being tested may be measured.

- Another technique for drug screening provides for high throughput screening of compounds
20 having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with TRICH, or fragments thereof, and washed. Bound TRICH is then detected by methods well known in the art. Purified TRICH can also be coated directly onto plates for use in the aforementioned drug screening techniques.
25 Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

- In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding TRICH specifically compete with a test compound for binding TRICH. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more
30 antigenic determinants with TRICH.

In additional embodiments, the nucleotide sequences which encode TRICH may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

5 The disclosures of all patents, applications and publications, mentioned above and below including U.S. Ser. No. 60/216,547, U.S. Ser. No. 60/218,232, U.S. Ser. No. 60/220,112, and U.S. Ser. No. 60/221,839 are expressly incorporated by reference herein., are expressly incorporated by reference herein.

10 **EXAMPLES**

I. Construction of cDNA Libraries

Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA
20 purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated
using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN,
Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was
isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA
purification kit (Ambion, Austin TX).

25 In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic
30 oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g.,

PBLUESCRIPT plasmid (Stratagene), PSORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4 °C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the

5 GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA

10 sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA.

15 The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein

20 family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent

25 identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of

30 which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:33-64. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 4.

5 **IV. Identification and Editing of Coding Sequences from Genomic DNA**

Putative transporters and ion channels were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin
10 (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode transporters and ion channels, the encoded polypeptides were analyzed by querying
15 against PFAM models for transporters and ion channels. Potential transporters and ion channels were also identified by homology to Incyte cDNA sequences that had been annotated as transporters and ion channels. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by
20 Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using
25 the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

"Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification
30 program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence.

Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then “stitched” together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants. Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpr public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

“Stretched” Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore “stretched” or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of TRICH Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:33-64 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:33-64 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences

had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, *supra*, ch. 7; Ausubel (1995) *supra*, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For

example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

5 Alternatively, polynucleotide sequences encoding TRICH are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system;
 10 embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer,
 15 cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding TRICH. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

20 **VIII. Extension of TRICH Encoding Polynucleotides**

Full length polynucleotide sequences were also produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to initiate 3' extension of the known fragment. The initial primers were designed using
 25 OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension
 30 was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme

(Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, full length polynucleotide sequences are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling and Use of Individual Hybridization Probes

- 5 Hybridization probes derived from SEQ ID NO:33-64 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine
- 10 triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or
- 15 Pvu II (DuPont NEN).

- The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate.
- 20 Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

X. Microarrays

- The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra.), mechanical
- 25 microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be
- 30 produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Skena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by *in vitro* transcription from non-coding yeast genomic DNA. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and
5 coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic
10 apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in
15 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with
20 an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide
30 containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477,
35 Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate

filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

5 The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different
10 fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

 The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC
15 computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

20 A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

25 Sequences complementary to the TRICH-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring TRICH. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of TRICH. To inhibit transcription, a
30 complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the TRICH-encoding transcript.

XII. Expression of TRICH

Expression and purification of TRICH is achieved using bacterial or virus-based expression systems. For expression of TRICH in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express TRICH upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of TRICH in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding TRICH by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, TRICH is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from TRICH at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified TRICH obtained by these methods can be used directly in the assays shown in Examples XVI, XVII, and XVIII where applicable.

30 XIII. Functional Assays

TRICH function is assessed by expressing the sequences encoding TRICH at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which

contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of TRICH on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding TRICH and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding TRICH and other genes of interest can be analyzed by northern analysis or microarray techniques.

XIV. Production of TRICH Specific Antibodies

TRICH substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the TRICH amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch¹¹.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the
5 oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-TRICH activity by, for example, binding the peptide or TRICH to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XV. Purification of Naturally Occurring TRICH Using Specific Antibodies

Naturally occurring or recombinant TRICH is substantially purified by immunoaffinity
10 chromatography using antibodies specific for TRICH. An immunoaffinity column is constructed by covalently coupling anti-TRICH antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing TRICH are passed over the immunoaffinity column, and the column is
15 washed under conditions that allow the preferential absorbance of TRICH (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/TRICH binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and TRICH is collected.

XVI. Identification of Molecules Which Interact with TRICH

20 Molecules which interact with TRICH may include transporter substrates, agonists or antagonists, modulatory proteins such as G β y proteins (Reimann, *supra*) or proteins involved in TRICH localization or clustering such as MAGUKs (Craven, *supra*). TRICH, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate
25 are incubated with the labeled TRICH, washed, and any wells with labeled TRICH complex are assayed. Data obtained using different concentrations of TRICH are used to calculate values for the number, affinity, and association of TRICH with the candidate molecules.

Alternatively, proteins that interact with TRICH are isolated using the yeast 2-hybrid system (Fields, S. and O. Song (1989) Nature 340:245-246). TRICH, or fragments thereof, are expressed as
30 fusion proteins with the DNA binding domain of Gal4 or lexA, and potential interacting proteins are expressed as fusion proteins with an activation domain. Interactions between the TRICH fusion protein and the TRICH interacting proteins (fusion proteins with an activation domain) reconstitute a transactivation function that is observed by expression of a reporter gene. Yeast 2-hybrid systems are

commercially available, and methods for use of the yeast 2-hybrid system with ion channel proteins are discussed in Niethammer, M. and M. Sheng (1998, Meth. Enzymol. 293:104-122).

TRICH may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions
5 between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

Potential TRICH agonists or antagonists may be tested for activation or inhibition of TRICH ion channel activity using the assays described in section XVIII.

XVII. Demonstration of TRICH Activity

10 Ion channel activity of TRICH is demonstrated using an electrophysiological assay for ion conductance. TRICH can be expressed by transforming a mammalian cell line such as COS7, HeLa or CHO with a eukaryotic expression vector encoding TRICH. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. A second plasmid which expresses any one of a number of marker genes, such as β -
15 galactosidase, is co-transformed into the cells to allow rapid identification of those cells which have taken up and expressed the foreign DNA. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression and accumulation of TRICH and β -galactosidase.

Transformed cells expressing β -galactosidase are stained blue when a suitable colorimetric
20 substrate is added to the culture media under conditions that are well known in the art. Stained cells are tested for differences in membrane conductance by electrophysiological techniques that are well known in the art. Untransformed cells, and/or cells transformed with either vector sequences alone or β -galactosidase sequences alone, are used as controls and tested in parallel. Cells expressing TRICH will have higher anion or cation conductance relative to control cells. The contribution of TRICH to
25 conductance can be confirmed by incubating the cells using antibodies specific for TRICH. The antibodies will bind to the extracellular side of TRICH, thereby blocking the pore in the ion channel, and the associated conductance.

Alternatively, ion channel activity of TRICH is measured as current flow across a TRICH-containing Xenopus laevis oocyte membrane using the two-electrode voltage-clamp technique (Ishi et
30 al., supra; Jegla, T. and L. Salkoff (1997) J. Neurosci. 17:32-44). TRICH is subcloned into an appropriate Xenopus oocyte expression vector, such as pBF, and 0.5-5 ng of mRNA is injected into mature stage IV oocytes. Injected oocytes are incubated at 18°C for 1-5 days. Inside-out macropatches are excised into an intracellular solution containing 116 mM K-gluconate, 4 mM KCl, and 10 mM Hepes (pH 7.2). The intracellular solution is supplemented with varying concentrations
35 of the TRICH mediator, such as cAMP, cGMP, or Ca^{+2} (in the form of CaCl_2), where appropriate.

Electrode resistance is set at 2-5 M Ω and electrodes are filled with the intracellular solution lacking mediator. Experiments are performed at room temperature from a holding potential of 0 mV. Voltage ramps (2.5 s) from -100 to 100 mV are acquired at a sampling frequency of 500 Hz. Current measured is proportional to the activity of TRICH in the assay.

- 5 In particular, the activities of TRICH-1, TRICH-2, and TRICH-10, are measured as K⁺ conductance, the activities of TRICH-6 and TRICH-9 are measured as K⁺ conductance in the presence of membrane stretch or free fatty acids, the activities of TRICH-18, TRICH-25 and TRICH-31 are measured as voltage-gated K⁺ conductance, TRICH-5 activity is measured as Cl⁻ conductance in the presence of GABA, TRICH-11 activity is measured as cation conductance in the presence of heat, and
10 the activity of TRICH-9, TRICH-28 is measured as Ca²⁺ conductance.

- Transport activity of TRICH is assayed by measuring uptake of labeled substrates into *Xenopus laevis* oocytes. Oocytes at stages V and VI are injected with TRICH mRNA (10 ng per oocyte) and incubated for 3 days at 18°C in OR2 medium (82.5mM NaCl, 2.5 mM KCl, 1mM CaCl₂, 1mM MgCl₂, 1mM Na₂HPO₄, 5 mM Hepes, 3.8 mM NaOH, 50 μ g/ml gentamycin, pH 7.8) to allow
15 expression of TRICH. Oocytes are then transferred to standard uptake medium (100mM NaCl, 2 mM KCl, 1mM CaCl₂, 1mM MgCl₂, 10 mM Hepes/Tris pH 7.5). Uptake of various substrates (e.g., amino acids, sugars, drugs, ions, and neurotransmitters) is initiated by adding labeled substrate (e.g. radiolabeled with ³H, fluorescently labeled with rhodamine, etc.) to the oocytes. After incubating for 30 minutes, uptake is terminated by washing the oocytes three times in Na⁺-free medium, measuring the
20 incorporated label, and comparing with controls. TRICH activity is proportional to the level of internalized labeled substrate. In particular, test substrates include pigment precursors and related molecules for TRICH-3, aminophospholipids for TRICH-4, fructose and glucose for TRICH-7 and TRICH-15, amino acids for TRICH-8, Na⁺ and iodide for TRICH-12, Na⁺ and H⁺ for TRICH-13 and TRICH-21, Na⁺ and glucose for TRICH-16 and TRICH-19, and glucose for TRICH-23, TRICH-26,
25 TRICH-29, TRICH-30, and TRICH-32.

- ATPase activity associated with TRICH can be measured by hydrolysis of radiolabeled ATP-[γ -³²P], separation of the hydrolysis products by chromatographic methods, and quantitation of the recovered ³²P using a scintillation counter. The reaction mixture contains ATP-[γ -³²P] and varying amounts of TRICH in a suitable buffer incubated at 37°C for a suitable period of time. The reaction is
30 terminated by acid precipitation with trichloroacetic acid and then neutralized with base, and an aliquot of the reaction mixture is subjected to membrane or filter paper-based chromatography to separate the reaction products. The amount of ³²P liberated is counted in a scintillation counter. The amount of radioactivity recovered is proportional to the ATPase activity of TRICH in the assay.

XVIII. Identification of TRICH Agonists and Antagonists

TRICH is expressed in a eukaryotic cell line such as CHO (Chinese Hamster Ovary) or HEK (Human Embryonic Kidney) 293. Ion channel activity of the transformed cells is measured in the presence and absence of candidate agonists or antagonists. Ion channel activity is assayed using patch clamp methods well known in the art or as described in Example XVII. Alternatively, ion channel

5 activity is assayed using fluorescent techniques that measure ion flux across the cell membrane (Velicelebi, G. et al. (1999) *Meth. Enzymol.* 294:20-47; West, M.R. and C.R. Molloy (1996) *Anal. Biochem.* 241:51-58). These assays may be adapted for high-throughput screening using microplates. Changes in internal ion concentration are measured using fluorescent dyes such as the Ca^{2+} indicator Fluo-4 AM, sodium-sensitive dyes such as SBFI and sodium green, or the Cl^- indicator MQAE (all

10 available from Molecular Probes) in combination with the FLIPR fluorimetric plate reading system (Molecular Devices). In a more generic version of this assay, changes in membrane potential caused by ionic flux across the plasma membrane are measured using oxonyl dyes such as DiBAC₄ (Molecular Probes). DiBAC₄ equilibrates between the extracellular solution and cellular sites according to the cellular membrane potential. The dye's fluorescence intensity is 20-fold greater when bound to

15 hydrophobic intracellular sites, allowing detection of DiBAC₄ entry into the cell (Gonzalez, J.E. and P.A. Negulescu (1998) *Curr. Opin. Biotechnol.* 9:624-631). Candidate agonists or antagonists may be selected from known ion channel agonists or antagonists, peptide libraries, or combinatorial chemical libraries.

20 Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious

25 to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
3474673	1	3474673CD1	33	3474673CB1
4588877	2	4588877CD1	34	4588877CB1
7472214	3	7472214CD1	35	7472214CB1
7473053	4	7473053CD1	36	7473053CB1
7473347	5	7473347CD1	37	7473347CB1
7474240	6	7474240CD1	38	7474240CB1
7475338	7	7475338CD1	39	7475338CB1
7476747	8	7476747CD1	40	7476747CB1
7477898	9	7477898CD1	41	7477898CB1
7472728	10	7472728CD1	42	7472728CB1
7474322	11	7474322CD1	43	7474322CB1
5455621	12	5455621CD1	44	5455621CB1
7477248	13	7477248CD1	45	7477248CB1
2944004	14	2944004CD1	46	2944004CB1
3046849	15	3046849CD1	47	3046849CB1
4538363	16	4538363CD1	48	4538363CB1
6427460	17	6427460CD1	49	6427460CB1
7474127	18	7474127CD1	50	7474127CB1
7476949	19	7476949CD1	51	7476949CB1
7477249	20	7477249CD1	52	7477249CB1
7477720	21	7477720CD1	53	7477720CB1
7477852	22	7477852CD1	54	7477852CB1
1471717	23	1471717CD1	55	1471717CB1
3874406	24	3874406CD1	56	3874406CB1
4599654	25	4599654CD1	57	4599654CB1
5047435	26	5047435CD1	58	5047435CB1
7475603	27	7475603CD1	59	7475603CB1
7477845	28	7477845CD1	60	7477845CB1
168827	29	168827CD1	61	168827CB1
7472734	30	7472734CD1	62	7472734CB1
7473473	31	7473473CD1	63	7473473CB1
7477725	32	7477725CD1	64	7477725CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
1	3474673CD1	g13507377	1.00E-151	[fl][Homo sapiens] potassium channel TASK-4 (Decher,N. et al. (2001) FEBS Lett. 492 (1-2), 84-89)
2	4588877CD1	g13926111	3.00E-96	[fl][Homo sapiens] (AF358910) 2P domain potassium channel Talk-2
3	7472214CD1	g1107730	1.70E-243	[Mus musculus] ABC8
		g11342541	0	(Savary,S. et al. (1996) Mamm. Genome 7 (9), 673-676)
				[fl][Homo sapiens] putative white family ATP-binding cassette transporter
4	7473053CD1	g3850108	9.00E-209	[Schizosaccharomyces pombe] putative calcium- transporting atpase
		g3628757	0	[Homo sapiens] FIC1
5	7473347CD1	g1060975	1.70E-206	(Bull,L.N. et al. (1998) Nat. Genet. 18 (3), 219-224)
				[Rattus norvegicus] GABA receptor rho-3 subunit precursor
6	7474240CD1	g2745727	0	(Ogurusu,T. et al. (1996) Biochim. Biophys. Acta 1305 (1-2), 15-18)
7	7475338CD1	g183298	2.10E-158	[Rattus norvegicus] potassium channel
				(Shi,W. et al. (1997) J. Neurosci. 17 (24), 9423-9432)
9	7477898CD1	g2745729	0	[Homo sapiens] GLUT5 protein
10	7472728CD1	g8452900	3.50E-261	(Kayano,T. et al. (1990) J. Biol. Chem. 265 (22), 13276-13282)
				[Rattus norvegicus] potassium channel
11	7474322CD1	g12003146	0	(Shi,W. et al. (1997) J. Neurosci. 17 (24), 9423-9432)
12	5455621CD1	g1399954	3.00E-143	[Rattus norvegicus] potassium channel TREK-2
13	7477248CD1	g2944233	3.10E-195	(Bang,H. et al. (2000) J. Biol. Chem. 275 (23), 17412- 17419)
				[fl][Homo sapiens] capsaicin receptor
				[Rattus norvegicus] thyroid sodium/iodide symporter NIS
				(Dai,G. et al. (1996) Nature 379 (6564), 458-460)
				[Homo sapiens] sodium-hydrogen exchanger 6
				(Numata,M. et al. (1998) J. Biol. Chem. 273 (12), 6951- 6959)
14	2944004CD1	g3451312	1.40E-188	[Schizosaccharomyces pombe] membrane atpase
15	3046849CD1	g12802047	0	[fl][Homo sapiens] (AJ271290) facilitative glucose transporter GLUT11

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
16	4538363CD1	g338055	7.40E-181	[Homo sapiens] Na ⁺ /glucose cotransporter (Hediger, M.A. et al. (1989) Proc. Natl. Acad. Sci. U.S.A. 86 (15), 5748-5752)
17	6427460CD1	g6457274	0	[Mus musculus] putative E1-E2 ATPase (Hallock, M.S. et al. (1999) Physiol. Genomics (Online) 1 (3), 139-150)
18	7474127CD1	g206044	0	[Rattus norvegicus] potassium channel Kv3.2b (Wiedemann, R. et al. (1991) FEBS Lett. 288, 163-167)
19	7476949CD1	g9588428	0	[5' incm] [Homo sapiens] dJ1024N4.1 (novel Sodium: solute symporter family member similar to SLC5A1 (SGLT1))
20	7477249CD1	g338055	3.70E-202	[Homo sapiens] Na ⁺ /glucose cotransporter (Hediger, M.A. et al. (1989) Proc. Natl. Acad. Sci. U.S.A. 86 (15), 5748-5752)
21	7477200CD1	g7715417	0	[Oryctolagus cuniculus] RING-finger binding protein (Mansharamani, M. et al. (2001) J. Biol. Chem. 276 (5), 3641-3649)
22	7477852CD1	g205709	0	[Rattus norvegicus] sodium-hydrogen exchange protein- isoform 4 (Orlowski, J. et al. (1992) J. Biol. Chem. 267, 9331- 9339)
23	1471717CD1	g8920219	0	[fl] [Homo sapiens] epithelial calcium channel (Muller, D. et al. (2000) Genomics 67 (1), 48-53)
24	3874406CD1	g529590	5.00E-36	[Rattus norvegicus] liver-specific transport protein (Simonson, G.D. et al. (1994) J. Cell. Sci. 107, 1065- 1072)
25	4599654CD1	g1514530	1.90E-117	[Homo sapiens] ABC-C transporter (Klugbauer, N. et al. (1996) FEBS Lett. 391 (1-2), 61- 65)
		g3242244	0	[Mus musculus] hyperpolarization-activated cation channel, HAC3 (Ludwig, A. et al. (1998) Nature 393 (6685), 587-591)

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
26	5047435CD1	g13445575	0	[fl][Homo sapiens] facilitative glucose transporter GLUT10 (McVie-Wylie, A.J. et al. (2001) Genomics 72 (1), 113- 117)
27	7475603CD1	g9211112	0	[fl][Homo sapiens] macrophage ABC transporter (Kaminski, W.E. et al. (2000) Biochem. Biophys. Res. Commun. 273 (2), 532-538)
28	7477845CD1	g3800830	0	[Rattus norvegicus] putative four repeat ion channel (Lee, J.H. et al. (1999) FEBS Lett. 445 (2-3), 231-236)
29	168827CD1	g7707622	1.20E-116	[Homo sapiens] organic anion transporter 4 (Cha, S.H. et al. (2000) J. Biol. Chem. 275 (6), 4507- 4512)
30	7472734CD1	g3004482	0	[fl][Rattus norvegicus] putative integral membrane transport protein (Schomig, E. et al. (1998) FEBS Lett. 425 (1), 79-86)
		g7707622	4.50E-117	[Homo sapiens] organic anion transporter 4 (Cha, S.H. et al. (2000) J. Biol. Chem. 275 (6), 4507- 4512)
		g3004482	0	[fl][Rattus norvegicus] putative integral membrane transport protein (Schomig, E. et al. (1998) FEBS Lett. 425 (1), 79-86)
31	7473473CD1	g6625694	0	[Rattus norvegicus] potassium channel Eag2 (Saganich, M.J. et al. (1999) J. Neurosci. 19 (24), 10789-10802)
32	7477725CD1	g3004482	1.00E-177	[fl][Rattus norvegicus] putative integral membrane transport protein
		g7707622	4.20E-130	(Schomig, E. et al. (1998) FEBS Lett. 425 (1), 79-86) [Homo sapiens] organic anion transporter 4 (Cha, S.H. et al. (2000) J. Biol. Chem. 275 (6), 4507- 4512)

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	3474673CD1	332	S201 S207 S234 S265 S280 S281 S289 S51 T169 T67	N65 N94	Transmembrane domains: R130-M155, V245-L264 TASK K+ channel domain: V14-S332	HMMER HMMER_PFAM
2	4588877CD1	226	S101 S128 S159 S174 S175 S183 S95		Transmembrane domain: V139-L158 CHANNEL PROTEIN IONIC POTASSIUM SUBUNIT K+ PUTATIVE SUBFAMILY K MEMBER PD021430: A78-E162	HMMER BLAST_PRODUM
3	7472214CD1	646	S143 S229 S261 S340 S341 S463 S554 S57 S644 S69 S89 T138 T157 T23 T472 T500 T591	N169 N422	Transmembrane domains: S430-M450, W564-D589, M618-V637 ABC transporter domain: R95-G277 ABC transporters family signature BL00211: I100-F111, L201-D232 ABC transporters family signature: V181-D232 PROTEIN TRANSMEMBRANE TRANSPORT ATPBINDING TRANSPORTER MEMBRANE ABC GLYCOPROTEIN INNER PUTATIVE PD000633: T365-Y583 do WHITE; FRUIT; FLY; SCARLET; DM05200 P45844 289-650: G277-L623 ABC TRANSPORTERS FAMILY DM00008 P45844 73-287: I61-Q276 ABC transporter motif: L201-L215 ATP/GTP binding site (P-loop): G102-S109	HMMER HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN BLAST_PRODUM BLAST_DOMO BLAST_DOMO MOTIFS MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
4	7473053CD1	1190	S153 S259 S268 S391 S413 S452 S493 S545 S573 S624 S631 S687 S723 S739 S744 S832 S1174 S1132 S1164 S1124 S1143 S1168 T267 T36 T370 T378 T514 T519 T580 T646 T705 T732 T899 T980 T1098 T1158 Y23 Y29 Y489 Y607	N579	Transmembrane domains: S77-V94, L276-W298, Y330-R350, L947-I971, Q991-I1009 E1-E2 ATPase domains: E381-V403, Q530-A562, Y633-G685, R788-D818 E1-E2 ATPases phosphorylation site proteins BL00154: G134-L151, V386-F404, D650-M690, T809-S832 E1-E2 ATPases phosphorylation site: A372-V417 P-type cation-transporting ATPase superfamily signature PR00119: F390-F404, A666-D676, I812-I831 ATPASE HYDROLASE TRANSMEMBRANE PHOSPHORYLATION ATPBINDING PROTEIN PROBABLE CALCIUMTRANSPORTING CALCIUM TRANSPORT PD004657: S846-P1093 FIC1 PROTEIN PD180313: H1039-W1165 do ATPASE; CALCIUM; TRANSPORTING; DM02405 P32660 318-1225: W128-F418, E466-N910 ATPase E1-E2 motif: D392-T398	HMMER HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN BLIMPS_PRINTS BLAST_PRODROM BLAST_DOMO MOTIFS
5	7473347CD1	467	S149 S175 S344 S37 S390 S411 S419 S427 S53 S96 T100 T136 T157 T355 T356 T366 T41	N126 N197 N220	Transmembrane domain: V332-V351	HMMER

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5					Neurotransmitter-gated ion-channel domain: P58-Q362, H441-W463	HMMER_PFAM
					Neurotransmitter-gated ion channels signature BL00236: V85-P122, I139-H148, D169-Y207, Y254-A295	BLIMPS_BLOCKS
					Neurotransmitter-gated ion-channels signature: L164-H218	PROFILESKAN
					Neurotransmitter-gated ion-channels signature PR00252: T105-F121, K138-S149, C184-C198, S261-P273	BLIMPS_PRINTS
					Gamma-aminobutyric acid A (GABAA) receptor signature PR00253: F270-W290, V296-V317, V330-V351, Y446-Y466	BLIMPS_PRINTS
					CHANNEL IONIC TRANSMEMBRANE GLYCOPROTEIN POSTSYNAPTIC MEMBRANE RECEPTOR PRECURSOR SIGNAL PROTEIN PD000153: E62-S427	BLAST_PRODOR
					NEUROTRANSMITTER-GATED ION-CHANNELS DM00560 P50573 34-464: S37-V467	BLAST_DOMO
					Neurotransmitter-gated ion channels motif: C184-C198	MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
6	7474240CD1	1196	S174 S187 S209 S211 S239 S269 S274 S275 S317 S349 S354 S514 S55 S609 S639 S821 S869 S879 S883 S896 S899 S906 S922 S923 S939 S940 S963 S974 S985 S1020 S1091 S1170 S1096 T133 T169 T344 T371 T392 T528 T582 T637 T673 T74 T829 T857 T916 T1022 T1027 T1134 T1099 Y248 Y446 Y98	N102 N230 N338 N369 N600 N661 N736 N881 N905 N1139	Transmembrane domain: V551-Y571 Transmembrane region cyclic nucleotide gated ion channel: Y492-I731 Cyclic nucleotide-binding domain: M759-E850 POTASSIUM CHANNEL IONIC CHANNEL PD104127: S852-Y1028 POTASSIUM CHANNEL IONIC CHANNEL PD104126: A1076-K1196 CAMP RECEPTOR PROTEIN CYCLIC NUCLEOTIDE-BINDING DOMAIN DM01165 I38465 562-948: H564-A914 do POTASSIUM; CHANNEL; KST1; AKT1; DM02383 I38465 353-560: S353-A563 do CHANNEL; POTASSIUM; EAG; DM05484 I38465 1-351: M1-P351	HMMER HMMER_PFAM HMMER_PFAM BLAST_PRODUM BLAST_PRODUM BLAST_DOMO BLAST_DOMO
7	7475338CD1	512	S222 S279 S412 S413 S438 T107 T170 T235 T247 T473 T59 T66 Y380	N41 N57	Signal peptide: M1-A35 Transmembrane domains: C79-G96, M171-L188, Y322-V342, F448-I466 Sugar (and other) transporter domain: A26-F481 Sugar transport proteins signatures: A119-I185, V323-S379 Sugar transporter signature PR00171: A35-V45, V135-M154, Q294-Y304, I383-V404, T406-F418 Glucose transporter signature PR00172: L284-Y305, Q321-V342, L352-Q372, I383-T406, A416-F434, Y446-I466	SPSCAN HMMER HMMER_PFAM PROFILES SCAN BLIMPS_PRINTS BLIMPS_PRINTS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
7					SUGAR TRANSPORT PROTEINS DM00135 P22732 132-466: R138-T473 Sugar transporter 1 motif: S338-A353 Sugar transporter 2 motif: V140-R165	BLAST_DOMO MOTIFS MOTIFS
8	7476747CD1	568	S143 S365 S4 S456 S46 S51 S55 T34 T430 Y45	N141 N205 N214 N256 N562 N62 N76	Transmembrane domains: I242-F269, Y289-P308, I322-Y342 Transmembrane amino acid transporter protein domain: A102-G543 ACID AMINO PROTEIN TRANSPORTER PERMEASE TRANSMEMBRANE INTERGENIC REGION PUTATIVE PROLINE PD001875: W80-L380 Transmembrane domain: L300-N318	HMMER HMMER_PFAM BLAST_PRODUM
9	7477898CD1	958	S105 S140 S145 S200 S26 S283 S288 S458 S488 S55 S670 S706 S724 S751 S774 S788 S864 S872 S879 S897 S929 T13 T170 T202 T220 T301 T326 T363 T377 T486 T522 T678	N218 N449 N510 N742	Transmembrane region cyclic nucleotide gated ion channel: Y341-I580 Cyclic nucleotide-binding domain: V608-A699 POTASSIUM CHANNEL IONIC CHANNEL PD118772: E702-S955 CHANNEL PROTEIN IONIC POTASSIUM NONPHOTOTROPIC HYPOCOTYL PUTATIVE SUBUNIT REPEAT EAG PD009483: M1-L86 CAMP RECEPTOR PROTEIN CYCLIC NUCLEOTIDE-BINDING DOMAIN DM01165 I38465 562-948: H413-F738, do POTASSIUM; CHANNEL; KST1; AKT1; DM02383 I38465 353-560: T201-A412	HMMER HMMER_PFAM HMMER_PFAM BLAST_PRODUM BLAST_PRODUM BLAST_DOMO BLAST_DOMO

Table 3 (cont.)

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
10	7472728CD1	724	S229 S283 S303 S333 S512 S545 S597 S666 S718 T104 T19 T223 T444 T515 T540 T557 T591 T636 T640 T650 T661 T676	N327 N330 N331 N532 N664 N684 N716	Transmembrane domains: A370-L388, I419-F437, V486-M503 TASK K+ channel domain: M250-D646 TWIK1 RELATED POTASSIUM CHANNEL, SUBFAMILY K, MEMBER 2 TREK1 K+ CHANNEL SUBUNIT IONIC CHANNEL PD085853: P215-G326 Transmembrane domains: F62-Y87, F139-F163, F212-L230, I293-I312 VANILLOID RECEPTOR SUBTYPE 1 PD137334: C348-K470	HMMER HMMER_PFAM BLAST_PRODROM
11	7474322CD1	470	S134 S142 S245 S326 S355 S408 S411 S415 S432 S452 T15 T22 T229 T265 T337 T341 T36	N236 N256 N321 N380	Transmembrane domains: D10-F28, F81-Y104, F278-M297, L439-Y459, I502-R528 Sodium: solute symporter family domain: F41-G445 Sodium: solute symporter signature BL00456: T154-G208 Sodium: solute symporter family signature: N151-T198	HMMER BLIMPS_BLOCKS PROFILES CAN
12	5455621CD1	618	S110 S265 S313 S373 S490 S550 S565 S576 S594 T154 T237 T268 T360 T37 T526 T567 T70	N219 N256 N480 N574	TRANSMEMBRANE TRANSPORT PERMEASE PROTEIN SODIUM SYMPORT PROLINE COTRANSPORTER SYMPORTER GLYCOPROTEIN PD000991: F41-C304 SYMPORTER SODIUM IODIDE THYROID SODIUM/IODIDE NIS PD024705: I446-L489, S490-G575 SODIUM: SOLUTE SYMPORTER FAMILY DM00745 P31636 24-561: D10-N219, G220-Y459	BLAST_PRODROM BLAST_PRODROM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
13	7477248CD1	631	S149 S212 S258 S522 S9 T518 T551 T73 T79 Y14	N352 N516 N96	Transmembrane domains: V22-F41, L159-M181, I391-A407 Sodium/hydrogen exchanger family domain: L25-V491 Na+/H+ exchanger isoform 6 signature PR01088: Y14-I38, W39-V57, Y58-V84, Q119-E132, A269-M288, T480-Q506, K515- D533, P539-Q567, P566-E593 Na+/H+ exchanger signature PR01084: I133-F144, G147-S161, I162- T170, G208-T218 + TRANSPORT EXCHANGER NA PD01672: I133-M181 NA+/H+ PROTEIN TRANSMEMBRANE TRANSPORT ANTIPORTER SYMPORT SODIUM EXCHANGER GLYCOPROTEIN SODIUM/HYDROGEN PD000631: G20-G63, E132-R490 SODIUMHYDROGEN EXCHANGER 6 MYELOBLAST KIAA0267 PD177855: G478-Y591 do BETA; EXCHANGER; NA; DM02572 P48764 10-734: L124-L541 Transmembrane domains: Y231-Y251, L415-L434, I933-I959, F966- L985, I1002-F1020, N1104-M1122 E1-E2 ATPase domains: V274-V365, G490-D506, Q672-A785, L851- S899 E1-E2 ATPases phosphorylation site signature BL00154: V454-G490, L492-L510, K652- C662, N724-M764, V878-S901, A905-V938 E1-E2 ATPases phosphorylation site: I478-E526	HMMER HMMER_PPFAM BLIMPS_PRINTS BLIMPS_PRINTS BLIMPS_PRODOM BLAST_PRODOM BLAST_PRODOM BLAST_DOMO HMMER HMMER_PPFAM BLIMPS_BLOCKS PROFILES SCAN
14	2944004CD1	1256	S103 S130 S144 S170 S227 S252 S523 S802 S817 S899 S901 S98 S1055 T269 T353 T358 T387 T502 T549 T576 T74 T912 T1212 T1061 T1236 Y349 Y407	N150 N23 N300 N312 N318 N704 N1045 N1053 N1059 N1073 N1247		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
14					P-type cation-transporting ATPase superfamily signature PR00119: N318-T332, C496-L510, A740-D750, C881-L900 ATPASE PROBABLE CALCIUMTRANSPORTING PROTEIN HYDROLASE CALCIUM TRANSPORT TRANSMEMBRANE PHOSPHORYLATION MAGNESIUM PD090368: Q995-Y1094, D1064-L1114 E1-E2 ATPASES PHOSPHORYLATION SITE DM00115 P22189 49-801: S202-K331, P401-E505, S556-A575, V623-P767, H800-S984 E1-E2 ATPase motif: D498-T504	BLIMPS_PRINTS BLAST_PRODUM BLAST_DOMO
15	3046849CD1	499	S100 S118 S215 S285 T466 T487	N292 N34 N50	Signal peptide: M1-G27 Transmembrane domains: M163-L181, T371-G389, M418-L440 Sugar (and other) transporter signature: L18-L474 Sugar transport proteins signature: A112-V178 Sugar transporter signature PR00171: T28-I38, M128-M147, M376-L397, T399-C411 Glucose transporter signature PR00172: Q314-I335, M376-T399, A409-L427 SUGAR TRANSPORT PROTEINS DM00135 P22732 132-466: R131-T466 Sugar transporter 2 motif: L133-R158	MOTIFS SPSCAN HMMER HMMER_PFAM PROFILES SCAN BLIMPS_PRINTS BLIMPS_PRINTS BLAST_DOMO MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
16	4538363CD1	596	S17 S290 S39 S5 T119 T211	N239 N386 N4 N545 N96	Transmembrane domains: S73-W95, I185-I212, L356-A376, L410-V430, F473-F491, Y513-L533 Sodium:solute symporter family domain: Y50-G479 Sodium:solute symporter signature BL00456: Y27-G81, A103-R132, L165-G219, P452-G461 Sodium:solute symporter family signatures: H162-I209, V412-D502 TRANSMEMBRANE TRANSPORT PERMEASE PROTEIN SODIUM SYMPORT PROLINE COTRANSPORTER SYMPORTER GLYCOPROTEIN PD000991: Y50-G479 NA+/GLUCOSE COTRANSPORTERRELATED PROTEIN PD134393: L551-A596 NA+/GLUCOSE COTRANSPORTERRELATED PROTEIN PD166538: M1-G49 SODIUM:SOLUTE SYMPORTER FAMILY DM00745 P13866 24-561: S17-W548 Na solute symporter 2 motif: G461-V481	HMMER HMMER_PFAM BLIMPS_BLOCKS PROFILESAN BLAST_PRODUM BLAST_PRODUM BLAST_PRODUM BLAST_DOMO MOTIFS

Table 3 (cont.)

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
17	6427460CD1	1192	S143 S169 S188 S283 S287 S335 S451 S507 S508 S52 S555 S561 S722 S933 T203 T255 T259 T269 T333 T380 T413 T418 T659 T708 T714 T715 T910 T1103 T1017 T1105 Y885 Y1026	N397 N745 N921 N989 N1001	Transmembrane domains: V299-Y316, F1004-L1022, I1030-W1049, A1075-L1092 E1-E2 ATPase domains: E403-E425 I550-C698 E1-E2 ATPases phosphorylation site signature BL00154: G149-F166, V408-F426, D663-L703 E1-E2 ATPases phosphorylation site: L395-C442	HMMER HMMER_PFBM BLIMPS_BLOCKS PROFILES CAN BLIMPS_PRINTS BLAST_PRODROM
18	7474127CD1	638	S205 S224 S336 S378 S414 S541 S553 S564 S86 T120 T146 T155 T17 T21 T25 T283 T374 T49 T520 T546 T579	N259 N266 N518 N536 N84	PD004657: A857-V1108 do ATPASE; CALCIUM; TRANSPORTING; DM02405 Q09891 206-1107: T105-Y436, F471-N921 E1-E2 ATPase motif: D414-T420 Transmembrane domains: I231-L248, F382-Y401, M451-V473 Ion transport protein domain: L240-I472 Potassium channel signature PR00169: E101-T120, P222-T250, Y284-K307, F310-V330, F352-S378, E381-E404, F421-M443, G450-F476	MOTIFS HMMER HMMER_PFBM BLIMPS_PRINTS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
18					VOLTAGEGATED POTASSIUM CHANNEL PROTEIN KV3.2 KSHIIIA IONIC TRANSMEMBRANE ION TRANSPORT GLYCOPROTEIN MULTIGENE FAMILY ALTERNATIVE SPLICING PHOSPHORYLATION PD085814: K495-S538 do CHANNEL; POTASSIUM; CDRK; FORM; DM00436 P22462 189-350: R189-R351 do CHANNEL; POTASSIUM; CDRK; SHAW; DM00490 P22462 34-151: L34-C152	BLAST_PRODOM BLAST_DOMO BLAST_DOMO
19	7476949CDI	681	S307 S421 S56 S573 S582 S587 S638 S651 T422 T485 T650 Y510	N113 N251 N256 N403 N603	Transmembrane domains: I38-I57, S90-W112, I150-I167, L188-M207, L373-A393, V432-I448, Y530-L550 Sodium:solute symporter family domain: Y67-G496 Sodium:solute symporter signature BL00456: Y44-G98, A120-R149, L182-G236, P469-A478 Sodium:solute symporter family signatures: Q179-V226, D458-D519 TRANSMEMBRANE TRANSPORT PERMEASE PROTEIN SODIUM SYMPORT PROLINE COTRANSPORTER SYMPORTER GLYCOPROTEIN PD000991: Y67-G496 SODIUM:SOLUTE SYMPORTER FAMILY DM00745 P13866 24-561: H34-W565 Na solute symporter 1 motif: G183-A208	HMMER HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN BLAST_PRODOM BLAST_DOMO MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incye Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
20	7477249CD1	1096	S115 S163 S276 S280 S332 S333 S404 S454 S46 S461 S462 S508 S514 S671 S863 S891 S1084 T262 T340 T345 T347 T407 T570 T612 T687 T840 T948 T1034 T1036 Y322	N331 N383 N395 N411 N720 N932	Transmembrane domains: F289-L307, F935-L953, W967-V996, F1008-D1028 E1-E2 ATPase domains: T340-Q352, H502-V648 E1-E2 ATPases phosphorylation site signature BL00154: G143-L160, V335-F353, K529- C539, D616-H656 P-type cation-transporting ATPase superfamily signature PR00119: F339-F353, A632-D642 H+-transporting ATPase signature PR00120: T547-A565 ATPASE HYDROLASE TRANSMEMBRANE PHOSPHORYLATION ATPBINDING PROTEIN PROBABLE CALCIUMTRANSPORTING CALCIUM TRANSPORT PD004657: A787-K1038 do ATPASE; CALCIUM; TRANSPORTING; DM02405 P39524 236-1049: T83-I306, F422-N851 E1-E2 ATPase motif: D341-T347 Signal peptide: M1-A26 Transmembrane domains: I155-Y178, I271-T292, Sodium/hydrogen exchanger family domain: V73-K482 Na+/H+ exchanger signature PR01084: I158-A166, G200-A210, I129- L140, G143-S157	HMMER HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRINTS BLAST_PRODOR BLAST_DOMO MOTIFS SPSCAN HMMER HMMER_PFAM BLIMPS_PRINTS
21	7477720CD1	707	S204 S299 S360 S417 S488 S51 S58 S585 S591 S620 S638 S679 T334 T350 T483 T634 Y225 Y528	N297 N31 N342 N35		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
21					Na+/H+ exchanger isoform 2 (NHE2) signature PR01086: F115-S128, K616-I627 + TRANSPORT EXCHANGER NA PD01672: A83-I113, I129-L177, Y178-L212, A213-F249, D262-I287, S288-Y321, L322-M355, S359-F405, Y406-F452, I489-K531, I532-G562, R593-R640 NA+/H+ PROTEIN TRANSMEMBRANE TRANSPORT ANTIporter SYMPORT SODIUM EXCHANGER GLYCOPROTEIN SODIUM/HYDROGEN PD000631: I77-A438	BLIMPS_PRINTS BLIMPS_PRODUM
22	7477852CD1	729	S142 S144 S155 S285 S291 S299 S318 S654 S664 S669 S697 S719 T110 T138 T281 T379 T447 T532 T539	N208 N358 N717	do BETA; EXCHANGER; NA; DM02572 P26434 14-716: L15-L687 Transmembrane domains: F493-F512, M554-M570 Ankyrin repeats: L78-E108, A116-T148, F162-S194 VANILLOID RECEPTOR SUBTYPE 1 PD101189: F115-L220 ATP/GTP binding site (P-loop): A412-T419	BLAST_DOMO HMME HMME_PFAM BLAST_PRODUM
23	1471717CD1	492	S13 S18 S225 S314 S373 T323 T33 T351 T426	N229 N249	transmembrane domain: I48-V71, V86-F104, Y172-I199, I199-V217, F384-F402, V452-C472 Sugar (and other) transporter: I48-K492 SUGAR TRANSPORT PROTEINS DM00032 P30638 80-152:R45-K115 VESICLE; SYNAPTIC; SV2; FORM DM08835 S34961 180-344:I119-N249	MOTIFS HMME HMME_PFAM BLAST_DOMO BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
24	3874406CD1	1494	S30 S50 S134 S230 S368 S549 S638 S669 S686 S696 S792 S800 S831 S912 S1004 S1070 S1146 S1172 S1206 S1365 T111 T435 T449 T501 T520 T632 T649 T657 T729 T845 T1049 T1134 T1217 T1247 T1295 T1318 T1339 T1422 T1482 Y824	N109 N130 N313 N421 N453 N71 N788 N817 N84 N867 N91 N1182	transmembrane domain: L204-F221, T272-L290, L735-Y753, F896-S914, V941-I959, L975-R998, F1019-V1039 ABC transporter: G384-G566 G1190-G1366 ABC transporters family proteins BL00211: I389-L400, L492-D523 ABC transporters family signature: V472-D523 ABC TRANSPORTERS FAMILY DM00008 P41233 839-1045:I355-N565, K1177-M1363 DM00008 P34358 611-816:I355-N565, A1179-M1363 DM00008 P41233 1851-2058:K1173-S1365, I355-N565 DM00008 P23703 41-246:E1162-G1366, L377-G566 ATP/GTP-binding site motif A (P-loop): G391-S398, G1197-2004	HMMER HMMER_Pfam BLIMPS_BLOCKS PROFILES CAN BLAST_DOMO MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
25	4599654CD1	774	S355 S356 S40 S505 S552 S559 S597 S61 S67 S734 S736 T203 T418 T668 T764 Y490	N291 N416	transmembrane domain: Y95-F118, T203-L219, L327-L353 Transmembrane region cyclic Nucleotide G: Y168-I414 Cyclic nucleotide-binding domain: K443-M531 Cyclic nucleotide-binding domain proteins BL00888: G452-V475, G488-L497 cAMP-dependent protein kinase signature PR00103: F449-R463, S489-T498 HYPERPOLARIZATIONACTIVATED CATION CHANNEL, HAC3 PD180735: T538-M774 CHANNEL IONIC POTASSIUM K+ SUBUNIT HYPERPOLARIZATIONACTIVATED PROTEIN PUTATIVE EAG LONG PD001039: E74-R167 CAMP RECEPTOR PROTEIN CYCLIC NUCLEOTIDE-BINDING DOMAIN DM01165 A55251 333-706:H263-P561 DM01165 P29973 311-684:H263-P561 DM01165 Q03041 286-658:H263-G548 DM01165 S52072 262-635:H263-Q595	HMMER HMMER_PFAM HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLAST_PRODUM BLAST_PRODUM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
26	5047435CD1	614	S116 S210 S290 S538 S577 S606 T267 T432 T443 T591	N407 N599	transmembrane domain: V124-I142, A168-M190, A371-V390, W483-I511, S526-I543, F552-V570 Sugar (and other) transporter: L83-F585 Sugar transport proteins BL00216: L174-S223, G92-S103 Sugar transporter signature PR00171: G92-I102, V175-I194, L486-V507, S509-F521 Glucose transporter signature PR00172: V343-V364, L486-S509, R519-L537, W550-V570 Sugar_Transport_1: G138-G153 A360-A375 Sugar transport proteins signatures sugar_transport_1.prf: L344-S401 sugar_transport_2.prf: A160-A225 SUGAR TRANSPORT PROTEINS DM00135 S25015 122-478:A160-D417, L480-K574, DM00135 P09830 101-452:G161-V405, L481-K574 DM00135 Q01440 101-433:R178-G388, R178-G388, L486-G575 DM00135 P15729 242-463:A485-S577, R286-L414	HMMER HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRINTS MOTIFS PROFILES SCAN BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
27	7475603CD1	2180	S181 S216 S233 S260 S409 S419 S842 S983 S1008 S1172 S1229 S1237 S1269 S1349 S1353 S1462 S1469 S1504 S1566 S1881 S1993 S2018 S2174 S2167 T120 T165 T338 T348 T510 T599 T614 T822 T931 T1079 T1086 T1094 T1171 T1181 T1209 T1219 T1417 T1439 T1822 T1870 T1917 T1988 T2057 T2125 Y656 Y1448	N112 N132 N346 N374 N1100 N1415 N1420 N1491 N1552 N1695 N1831	transmembrane domain: F630-L648, L664-L680, V1570-V1590, M1622-Q1641 ABC transporter: G1854-G2035 G868-G1048 ABC transporters family BL00211: F873-T884, L974-D1005 ABC transporters family signature: A1940-D1991, D955-D1005 Abc_Transporter: L974-F988 ATP/GTP-binding site motif A (P-loop): G875-T882, G1861-T1868 ATPBINDING TRANSPORTER CASSETTE ABC TRANSPORT PROTEIN GLYCOPROTEIN TRANSMEMBRANE RIM ABCR PD005939: L1563-N1740 ATPBINDING TRANSPORTER CASSETTE ABC GLYCOPROTEIN TRANSMEMBRANE TRANSPORT ABCR RIM PD010118: R238-R514, L95-R243 ATPBINDING TRANSPORTER CASSETTE ABC GLYCOPROTEIN TRANSMEMBRANE TRANSPORT ABCR RIM SIMILARITY PD008845: P1307-E1560 ATPBINDING TRANSPORTER CASSETTE ABC GLYCOPROTEIN TRANSMEMBRANE TRANSPORT RIM ABCR SIMILARITY PD006867: L540-S685, D515-Q541	HMNER HMNER_PFAM BLIMPS_BLOCKS PROFILES SCAN MOTIFS MOTIFS BLAST_PROD OM BLAST_PROD OM BLAST_PROD OM BLAST_PROD OM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
27					ABC TRANSPORTERS FAMILY DM00008 P41233 839-1045:V841-A1046, L1829-M2032 DM00008 P41233 1851-2058:V1826-N2034, V841-V1045 DM00008 P34358 1441-1640:L1827-M2032, V843-V1045	BLAST_DOMO
28	7477845CD1	1737	S23 S254 S687 S692 S695 S7 S713 S766 S773 S8 S861 S1113 S1228 S1271 S1455 S1463 S1537 S1595 S1647 S1652 S1730 T272 T324 T886 T1257 T1320 T1359 T1387 T1406 T1456 T1486 T1528 T1561 T1570 T1645 T1694 Y419 Y702 Y832	N210 N216 N859 N1064 N1371 N1449	transmembrane domain: M1244-A1262, V1319-F1336, I1338-F1357, A1423-I1446, W107-V126, V181-M199, S298-I321, L509-V531, V575-I598, Y879-M904, I1017-F1034, I1134-V1152 Ion transport protein ion.trans: W32-I321 M380-I598 L884-V1155 I1206-I1446 Calcium channel signature PR00167: D535-D561 PROTEIN F17C8.6 C11D2.5 NEARLY IDENTICAL C ELEGANS PREDICTED PD023984: V1447-S1637, E1714-T1720 C11D2.6 PROTEIN PD178227: L1241-R1368, I1206-F1292 F585-E606 C11D2.6 PROTEIN SIMILARITY ALONG ENTIRE GENE CALCIUM CHANNEL ALPHA PROTEINS PD041964: L599-V885, CHANNEL CALCIUM IONIC SUBUNIT VOLTAGE GATED SODIUM ALPHA TRANSMEMBRANE L TYPE PD000032: Y887-V1120, I33-V330, K1361-F1450, I1206-F1357, I577-I598, F1337-L1356, I1134-F1159, D1416-V1443	HMMER HMMER_PPFAM BLIMPS_PRINTS BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM

Table 3 (cont.)

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
28					III REPEAT DM00079 A55138 1052-1268:V1020-L1227 DM00079 P35500 1424-1636:W1090-P1194, I1017-N1050	BLAST_DOMO
29	168827CD1	547	S109 S167 S201 S282 S336 S404 S408 S526 T133 T323 T35 T432 T453 T58	N102 N107 N56	IV REPEAT DM00277 P27732 1363-1572:F1337-L1536 DM00277 P15381 1384-1595:F1337-L1536 transmembrane domain: F16-T35, Y180-C200, S201-V222, M410- E429, T469-Y492, L496-L514 Sugar (and other) transporter: L13-Q528	BLAST_DOMO HMMER HMMER_PPFAM
30	7472734CD1	547	S143 S167 S201 S282 S336 S404 S408 S46 S526 S60 S68 T133 T323 T432 T453 T58	N102 N39 N56 N62	ORGANIC TRANSPORTERLIKE TRANSPORT PROTEIN RENAL ANION TRANSPORTER CATIONIC KIDNEYSPECIFIC SOLUTE PD151320: N102-L144 transmembrane domain: I18-F32, M147-Y163, Y180-C200, S201- V222, M410-E429, T469-Y492, L496-L514 Sugar (and other) transporter: L18-Q528 SUGAR TRANSPORT PROTEINS DM00032 P46501 280-351:V121-K173 ORGANIC TRANSPORTERLIKE TRANSPORT PROTEIN RENAL ANION TRANSPORTER CATIONIC KIDNEYSPECIFIC SOLUTE PD151320: N102-K145	BLAST_PRODUM HMMER HMMER_PPFAM BLAST_DOMO BLAST_PRODUM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
31	7473473CD1	988	S142 S237 S24 S252 S322 S369 S502 S680 S773 S847 S883 S925 S943 S952 S974 S981 T127 T14 T215 T442 T478 T521 T634 T725 T73 T832 T869 T909 T929	N170 N235 N403 N466 N663 N830	transmembrane domain: L342-A360 Transmembrane cyclic Nucleotide G: Y288-I536 Cyclic nucleotide-binding domain: V564-A655 PAC motif PA: C92-T132 CHANNEL POTASSIUM IONIC EAG SUBUNIT HEAG LONG ELECTROCARDIOGRAPHIC QT SYNDROME PD017645: K809-D984 CHANNEL IONIC K+ SUBUNIT HYPERPO- LARIZATION ACTIVATED PUTATIVE EAG LONG PD001039: S179-I284 CHANNEL K+ IONIC EAG SUBUNIT TRANSMEMBRANE ION TRANSPORT VOLTAGEGATED PD011550: N658-E737 CHANNEL PROTEIN IONIC POTASSIUM NON PHOTOTROPIC HYPOCOTYL PUTATIVE SUBUNIT REPEAT EAG PD009483: M1-E89 CAMP RECEPTOR PROTEIN CYCLIC NUCLEOTIDE- BINDING DOMAIN DM01165 I48912 391-786: H361-S756 DM01165 Q02280 384-776: H361-E737 DM01165 I38465 562-948: H361-R671, S974-E985 POTASSIUM; CHANNEL; KST1; AKT1; DM02383 I48912 164-389: V162-E314, E314-A360, W362-V455	HMMER HMMER_PFAM HMMER_PFAM HMMER_PFAM HMMER_PFAM BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
32	7477725CD1	533	S107 S109 S143 S167 S282 S345 S408 S469 S60 T133 T289 T323 T336 T432 T526	N102 N216 N56 N62	transmembrane domain: F150-D168, L380-N401, I407-V426, L486-F504 Sugar (and other) transporter: A111-K528 ORGANIC TRANSPORTER LIKE TRANSPORT PROTEIN RENAL ANION TRANSPORTER CATIONIC KIDNEY SPECIFIC SOLUTE PD151320: N102-K145	HMMER HMMER_PFAM BLAST_PRODOR

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
33	3474673CB1	1775	1-391, 578-786, 1024-1301	GNFL.g7798848_00000 3_004.edit 6724643H1 (LUNLFWT01) 3474673H1 (LUNGNOT27) 71495515V1 71495515V1 FL135171_00001 71497982V1 GBI:g8117242_000054 _edit.8639-8803 GBI:g8117242_000054 _edit.4857-4997 GBI:g8117242_000054 _edit.10305-10463 6891360H1 (BRAITDR03) GBI:g8117242_000054 _edit.50-89 GBI:g8117242_000054 _edit.6950-7093 GBI:g8117242_000054 _edit.4345-4478 60124962D2 GBI:g8117242_000054 _edit.8313-8414 GBI:g8118985_000043 _edit.12301- 12444.comp GBI:g8117242_000054 _edit.4112-4228 GBI:g8117242_000054 _edit.10957-11181 5500380H1 (BRABDIR01) GBI:g8117242_000054 _edit.10616-10732	1 861 249 1205 975 539 1 1171 544 1441 1433 1 925 358 1735 1069 685 241 1717 907 1600	1156 1347 568 1775 1545 1534 662 1335 684 1599 1905 240 1068 492 1941 1170 810 357 1941 1119 1716
34	4588877CB1	1545	261-619, 1-193, 794-1071			
35	7472214CB1	1941	1483-1558, 1- 413, 495-616, 732-1149			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
35				GBI:g8117242_000054 _edit.8907-9011	1336	1440
				GBI:g8117242_000054 _edit.6643-6756	811	924
36	7473053CB1	4971	3312-3482, 1- 1466, 4307-4971, 2184-2221	8035016J1 (SMCRUNE01)	2315	2975
				6822202J1 (SINTNOR01)	2145	2877
				6781747H1 (OVARDIR01)	968	1449
				8035016J1 (SMCRUNE01)	2979	3643
				6824230H1 (SINTNOR01)	2867	3483
				6894266H1 (BRAITDR03)	548	1157
				6777836H1 (OVARDIR01)	1601	2238
				6908503H1 (PITUDIR01)	1	667
				6908503J1 (PITUDIR01)	1270	1830
				6823447H1 (SINTNOR01)	3525	4260
				6823447J1 (SINTNOR01)	4226	4829
				6006310F8 (FIBRUNT02)	4501	4969
				4171959T6 (SINTNOT21)	3637	4287
				508860F6 (UTRSTMR01)	4461	4853
37	7473347CB1	1404	126-633, 1013- 1404, 768-838	GBI.lee4.edit	1	1404

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
38	7474240CB1	4048	3023-4048, 1753- 2469, 1-920, 1593-1658, 2614- 2908, 1138-1367	71984804V1 GBI:g7656646_edit 71986624V1 55055014H1 55037111J2 71983668V1 GBI:g5923734_edit 55037119J2 2502027F6 (ADRETUT05)	964 929 1369 1 95 1371 2612 224 696	1311 3418 1976 130 871 2043 4048 875 1235
39	7475338CB1	1539	1412-1539, 1- 328, 495-837, 922-1218	GBI:g7960701_000004 _edit.549-713 GBI:g7960701_000004 _edit.13381-13480 GBI:g7960701_000004 _edit.8755-8943 GBI:g7960701_000004 _edit.4292-4417 GBI:g7960701_000004 _edit.16237-16317 GBI:g7960701_000004 _edit.20107-20325 GBI:g7960701_000004 _edit.9989-10099 GBI:g7960701_000004 _edit.18748-18873 GBI:g7960701_000003 _edit.9783-9884 GBI:g7960701_000004 _edit.5251-5403 GBI:g7960701_000004 _edit.8384-8506 71906448V1 71753467V1	154 1015 715 313 1114 1321 904 1195 52 439 592 627 912	312 1113 903 438 1194 1539 1014 1320 153 591 714 1082 1539
40	7476747CB1	3114	1717-1870, 1- 503, 1468-1650	3351512F6 (PROSNOT28) 7761783J1 (THYMNOE02) 6934981R8 (SINTTMR02)	2185 1943 78	2724 2570 860

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
40				6389368H1 (PROSTMC01)	1782	2075
				70536163V1	2575	3114
				6934981F8 (SINTTMR02)	1	643
				GNN.g7712065_000012_002	452	1922
41	7477898CB1	2877	846-901, 1272-1378, 2319-2877	7080657H1 (STOMTMR02)	838	1403
42	7472728CB1	2820	1-1399, 2207-2229	5633289H1 (PLACFER01)	639	890
				g5746200	1215	1473
				GBI.g22262095	1	2877
				55022826J1	1138	1834
				55030210H1	403	986
				4399366T6 (TESTTUT03)	2231	2777
				55030274H1	1482	2153
				g565876	2597	2820
				55018149J1	1907	2585
				FL203597_00001	712	1807
				GNN.g7263861_026.ed it	1	1052
				GBI.g8081632_edit	1	1440
43	7474322CB1	1440	1-604, 714-768	71228887V1	1090	1440
44	5455621CB1	2394	1483-1686, 1-329, 838-1155, 2201-2235	70868623V1	988	1385
				3696546T6 (SININOT05)	1833	2394
				70674954V1	1520	2091
				1426382H1 (SINTBST01)	1224	1492
				3696546F6 (SININOT05)	799	1381
				6828352H1 (SINTNOR01)	530	1149
				3699565H1 (SININOT05)	1	281
				7700096H1 (KIDPTDE01)	250	990
				70678552V1	1419	2055

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
45	7477248CB1	2890	1-58, 2739-2890, 2310-2349, 329- 1167	2777287H1 (OVRTUT03) 7977733H1 (LSUBDMC01) 7678168J1 (NOSETUE01) 7611941J1 (KIDCTME01) 6590507H1 (TYMUNT03) 2701794F6 (OVRTUT10) 2544096F6 (UTRSNOT11) 6011704D2 5020832H1 (OVARNON03) 7662529H1 (UTRSTME01) 4762728F6 (PLACNOT05) 92264624 6264977H1 (MCLDTXN03) 2944004F6 (BRAITUT23) 6610392H2 (MUSTTMC01) GNN.97328818_000024 002.edit 7035078H1 (SINTFER03) 7620248J1 (HEARFEE03) 496537H1 (HNT2NOT01) 6264427T8 (MCLDTXN03) 6264427F8 (MCLDTXN03)	2250 841 1271 2273 179 1208 1732 1 2195 526 872 2268 1210 2790 3306 2145 1 2431 2329 453 170	2498 1427 1827 2890 672 1741 2252 431 2471 926 1387 2446 1797 3531 3926 2648 440 3039 2487 1174 842
46	2944004CB1	3926	3338-3365, 1- 687, 1222-2267			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
46				7673654H1 (FIBPFEC01)	1733	2239
47	3046849CB1	2135	2072-2135, 596- 711, 1014-1263	8262790UI 71896642V1 71247870V1 FL3046849_g6815043_ 000004_g183298	1383 1 1050 51	2135 592 1736 1520
48	4538363CB1	2637	1-183, 1575- 1680, 2094-2637	FL4538363_g3126781_ g520469 71401405V1 70857895V1 7727961J1 (UTRCDIE01) 70857789V1 g5689372_edit g3801917	1 1766 416 3284 566 1092 1	1917 2637 1035 3783 1109 3361 452
49	6427460CB1	3783	985-1833, 2687- 3204	GBI.g8568959_edit_3 g6140313 5819744F7 (PROTUS23) g5920552 55049678J1	1119 482 168 1 862	2105 951 479 488 1359
50	7474127CB1	2105	1078-2105	FL7476949_g6714723_ g338053 4669722H1 (SINTNOT24)	1 1801	2046 2069
51	7476949CB1	2069	1233-1356, 1- 117, 2047-2069, 347-503, 1536- 1844	71660072V1 71657569V1 7633968J1 (SINTDIE01) 6440145F8 (BRAENOT02) 71664080V1 GBI.g8567478_edit 71660176V1 71662066V1 2605539F6 (LUNGTFUT07) 71659261V1 3825558H1 (BRAIHCT02)	2404 3106 2579 938 3228 1 3773 1802 433 1690 1179	3156 3854 3175 1087 3891 2547 4245 2475 939 2437 1270
52	7477249CB1	4245	2833-3018, 1869- 2121, 3707-4245, 1-252, 982-1239, 289-357			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
52				7765571H1 (URETTUE01)	1	693
53	7477720CB1	2124	1-936, 1200- 1488, 1982-2124, 1562-1745	5675861H1 FL7477720_g5836195_ g205709	1427 1	1716 2124
54	7477852CB1	2195	1-418, 1899-2195	GBI.g8748866.edit	1	2195
55	1471717CB1	2055	206-768, 881- 931, 1155-1323	70464956V1 72277206V1 70469664V1 GNN.g7109510_000068 _002.edit GBI.g8039708_50_63_ 62_56.edit 6540941H1 (LNODNON02) 70466394V1	492 1 939 772 238 1571 1035	994 297 1582 1500 897 2055 1616
56	3874406CB1	4727	1-1299, 1576- 1632, 2550-3619, 2014-2192	71793833V1 55052105J1 71798347V1 71798870V1 55058313J1 55051482J1 FL3874406_g3810670_ g4240130_3_3-4 55068154H1 3133035F6 (SMCCNOT01) 55058329H1 55068182J1 71795307V1 8016331J1 (BMARTXE01) 71040001V1 8041905H1 (OVARTUE01) 55062505H1 g7959336_CD 6772024J1 (BRAUNOR01) 55064208J1	4117 1673 3620 3575 1380 2475 482 2223 1 723 2048 2902 1778 3348 1666 660 349 1 1118	4727 2128 4358 4244 2125 3134 744 2741 605 1528 2685 3593 2424 3852 2352 1233 2540 623 1718
57	4599654CB1	3852	1-335, 2014-3231			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
57				6617183H2 (BRAXTDR14) 6195941H1 (PITUNON01) 71909238V1 2216896F6 (SINTFET03) 71042073V1 7431853H1 (UTRMTMR02) GNN:g4375937_004_ed it 6426880H1 (LUNGNON07) 6781142H1 (OVARDIR01) 2645767H1 (OVARNOT09) 71704421V1 7726210H1 (THYRDIE01) 7721710J2 (THYRDIE01) 6340173F8 (BRANDIN01) 71704256V1 7757131H1 (SPLNTUE01) GNN:g7711543_000002 _002.edit 7464813H1 (LIVRFEE04) 71703676V1 7760618H1 (THYMN0E02) 71970086V1 7462584H1 (LIVRFEE04) 7760618J1 (THYMN0E02) 71762287V1	2981 2823 1225 2474 2276 1211 1 814 224 128 6240 1885 2696 5516 3025 2408 198 544 3250 2183 5817 1 1251 4313	3530 3458 1747 2923 2745 1917 1845 1336 941 394 6791 2602 3232 6222 3734 3093 2751 696 3947 2676 6525 578 1983 4879
58	5047435CB1	1917	1-238, 1162-1474			
59	7475603CB1	6791	1-3283, 5952- 6101, 3793-4761			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
59				7724639H1 (THYRDIE01)	951	1545
				55052451J1	4792	5698
				7739867H1 (THYMN0E01)	5131	5794
				6879936H1 (UTRSTMR02)	697	1054
60	7477845CB1	5214	2390-4599, 645- 1796	55058371H1	3850	4747
				GBI.g8346195_edit	1765	5214
				GBI.g8052096_edit	1132	1839
				8104845H1 (MIXDDIE02)	2822	3367
61	168827CB1	1818	1-281, 796-912	GBI.g8518014_edit	1	1266
				g1081430	1036	1525
				168827H1	65	406
				(LIVRNOT01)	1	209
				55054792J1	495	1110
				55072770H1	1321	1818
				GNN.g6498074_012.ed it		
				087510H1 (LIVRNOT01)	314	574
62	7472734CB1	2245	1223-1339, 1-710	g751568	1336	1773
				55055559H1	16	699
				55045003H2	1	697
				g5361744	908	1109
				GBI.g8118965_000015 _000006_000001_0000 10_000003.edit	602	2245
63	7473473CB1	3196	1-376, 460-1796	g751568	1763	2200
				55049235H1	556	1287
				GBI.g8018151_000001 .edit	1799	3196
				GBI.g6433826_000001 .edit	1172	2052
				55063069J1	1	850
				g669271	1799	2106

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
64	7477725CB1	1602	1072-1602	7455614H1 (LIVRTUE01)	416	835
				4288148H1 (LIVRDIR01)	112	257
				GBI.98131631_000007 _000005.edit	1	1602
				g2656651	829	1084

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
33	3474673CB1	LUNLTMT01
34	4588877CB1	LUNLTMT01
35	7472214CB1	BRAENOT04
36	7473053CB1	SINTNOR01
38	7474240CB1	ADRETUT05
39	7475338CB1	SINTNOT18
40	7476747CB1	SINTTMR02
42	7472728CB1	TESTTUT03
43	7474322CB1	SINTBST01
44	5455621CB1	SININOT05
45	7477248CB1	UTRSNOT11
46	2944004CB1	MCLDTXN03
47	3046849CB1	HNT2AGT01
48	4538363CB1	PANCNOT07
49	6427460CB1	BRAUNOR01
50	7474127CB1	PROSTUS23
51	7476949CB1	COLNTMC01
52	7477249CB1	COLNPOT01
55	1471717CB1	OVARDIT01
56	3874406CB1	LIVRDIR01
57	4599654CB1	LUNGNOT23
58	5047435CB1	OVARDIR01
59	7475603CB1	THYRDIE01
60	7477845CB1	MIXDDIE02
61	168827CB1	LIVRNOT01
64	7477725CB1	LIVRTUE01

Table 6

Library	Vector	Library Description
ADRETUT05	pINCY	Library was constructed using RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.
BRAENOT04	pINCY	Library was constructed using RNA isolated from inferior parietal cortex tissue removed from the brain of a 35-year-old Caucasian male who died from cardiac failure. Pathology indicated moderate leptomenigeal fibrosis and multiple microinfarctions of the cerebral neocortex. Patient history included dilated cardiomyopathy, congestive heart failure, cardiomegaly and an enlarged spleen and liver.
BRAUNOR01	pINCY	This random primed library was constructed using RNA isolated from striatum, globus pallidus and posterior putamen tissue removed from an 81-year-old Caucasian female who died from a hemorrhage and ruptured thoracic aorta due to atherosclerosis. Pathology indicated moderate atherosclerosis involving the internal carotids, bilaterally; microscopic infarcts of the frontal cortex and hippocampus; and scattered diffuse amyloid plaques and neurofibrillary tangles, consistent with age. Grossly, the leptomeninges showed only mild thickening and hyalinization along the superior sagittal sinus. The remainder of the leptomeninges was thin and contained some congested blood vessels. Mild atrophy was found mostly in the frontal poles and lobes, and temporal lobes, bilaterally. Microscopically, there were pairs of Alzheimer type II astrocytes within the deep layers of the neocortex. There was increased satellitosis around neurons in the deep gray matter in the middle frontal cortex. The amygdala contained rare diffuse plaques and neurofibrillary tangles. The posterior hippocampus contained a microscopic area of cystic cavitation with hemosiderin-laden macrophages surrounded by reactive gliosis. Patient history included sepsis, cholangitis, post-operative atelectasis, pneumonia CAD, cardiomegaly due to left ventricular hypertrophy, splenomegaly, arteriolonephrosclerosis, nodular colloidal goiter, emphysema, CHF, hypothyroidism, and peripheral vascular disease.
COLNPOT01	pINCY	Library was constructed using RNA isolated from colon polyp tissue removed from a 40-year-old Caucasian female during a total colectomy. Pathology indicated an inflammatory pseudopolyp; this tissue was associated with a focally invasive grade 2 adenocarcinoma and multiple tubovillous adenomas. Patient history included a benign neoplasm of the bowel.
COLNTMC01	pINCY	This large size-fractionated library was constructed using pooled cDNA from three different donors. cDNA was generated using mRNA isolated from colon epithelium tissue removed from a 13-year-old Caucasian female (donor A) who died from a motor vehicle accident; from ascending colon removed from a 29-year-old female (donor

Table 6 (cont.)

Library	Vector	Library Description
		B); and from colon tissue removed from the appendix of a 37-year-old Black female (donor C) during myectomy, dilation and curettage, right fimbrial region biopsy, and incidental appendectomy. Pathology for donor B indicated the proximal and distal resection margins of small bowel and colon away from the mass lesion were uninvolved by lymphoma. Pathology for donor C indicated an unremarkable appendix. Pathology for the matched tumor tissue (donor B) indicated malignant lymphoma, small cell, non-cleaved (Burkitt's lymphoma, B-cell phenotype), forming a polypoid mass in the region of the ileocecal valve, associated with intussusception and obstruction clinically. The liver and multiple (3 of 12) ileocecal region lymph nodes were also involved by lymphoma. Pathology for the associated tumor tissue (donor C) indicated multiple uterine leiomyomata. Donor C presented with deficiency anemia, an umbilical hernia, and premenopausal menorrhagia. Patient history included sarcoidosis of the lung.
HNT2AGT01	PBLUESCRIPT	Library was constructed at Stratagene (STR937233), using RNA isolated from the hNT2 cell line derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor. Cells were treated with retinoic acid for 5 weeks and with mitotic inhibitors for two weeks and allowed to mature for an additional 4 weeks in conditioned medium.
LIVRDIR01	pINCY	The library was constructed using RNA isolated from diseased liver tissue removed from a 63-year-old Caucasian female during a liver transplant. Patient history included primary biliary cirrhosis diagnosed in 1989. Serology was positive for anti-mitochondrial antibody.
LIVRNOT01	PBLUESCRIPT	Library was constructed at Stratagene, using RNA isolated from the liver tissue of a 49-year-old male.
LIVRTUE01	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from liver tumor tissue removed from a 72-year-old Caucasian male during partial hepatectomy. Pathology indicated metastatic grade 2 (of 4) neuroendocrine carcinoma forming a mass. The patient presented with metastatic liver cancer. Patient history included benign hypertension, type I diabetes, prostatic hyperplasia, prostate cancer, alcohol abuse in remission, and tobacco abuse in remission. Previous surgeries included destruction of a pancreatic lesion, closed prostatic biopsy, transurethral prostatectomy, removal of bilateral testes and total splenectomy. Patient medications included Euflexin, Hytrin, Proscar, Ecotrin, and insulin. Family history included atherosclerotic coronary artery disease and acute myocardial infarction in the mother; atherosclerotic coronary artery disease and type II diabetes in the father.
LUNGNOT23	pINCY	Library was constructed using RNA isolated from left lobe lung tissue removed from

Table 6 (cont.)

Library	Vector	Library Description
LJNL/TMT01	pINCY	<p>a 58-year-old Caucasian male. Pathology for the associated tumor tissue indicated metastatic grade 3 (of 4) osteosarcoma. Patient history included soft tissue cancer, secondary cancer of the lung, prostate cancer, and an acute duodenal ulcer with hemorrhage. Family history included prostate cancer, breast cancer, and acute leukemia.</p> <p>The library was constructed using RNA isolated from right middle lobe lung tissue removed from a 63-year-old Caucasian female during a segmental lung resection. Pathology for the associated tumor tissue indicated grade 3 adenocarcinoma in the right lower lobe and right middle lobe that infiltrated the parietal pleural surface. Metastatic grade 3 adenocarcinoma was found in the diaphragm. The lymph nodes contained metastatic grade 3 adenocarcinoma and involved the superior mediastinal and inferior mediastinal lymph nodes. Patient history included hyperlipidemia. Family history included benign hypertension, cerebrovascular disease, breast cancer, and hyperlipidemia.</p>
MCLDTXN03	pINCY	<p>This normalized dendritic cell library was constructed from one million independent clones from a pool of two derived dendritic cell libraries. Starting libraries were constructed using RNA isolated from untreated and treated derived dendritic cells from umbilical cord blood CD34+ precursor cells removed from a male. The cells were derived with granulocyte/macrophage colony stimulating factor (GM-CSF), tumor necrosis factor alpha (TNF alpha), and stem cell factor (SCF). The GM-CSF was added at time 0 at 100 ng/ml, the TNF alpha was added at time 0 at 2.5 ng/ml, and the SCF was added at time 0 at 25 ng/ml. Incubation time was 13 days. The treated cells were then exposed to phorbol myristate acetate (PMA), and Ionomycin. The PMA and Ionomycin were added at 13 days for five hours. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228-9232 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48 hours/round) reannealing hybridization was used.</p>
MIXDDIE02	PEK-CMV	<p>This 5' biased random primed library was constructed using pooled cDNA from seven donors. cDNA was generated using mRNA isolated from brain tissue removed from two Caucasian male fetuses who died after 23 weeks gestation from hypoplastic left heart (A) and prematurity (B); from posterior hippocampus from a 55-year-old male who died from COPD (C); from cerebellum, corpus callosum, thalamus and temporal lobe tissue from a 57-year-old Caucasian male who died from a CVA (D); from dentate nucleus and vermis from an 82-year-old Caucasian male who died from a myocardial infarction (E); from pituitary gland from a 74-year-old Caucasian female who died from a myocardial infarction (F) and vermis tissue from a 77-year-old Caucasian female who died from pneumonia (G). For donor C, pathology indicated</p>

Table 6 (cont.)

Library	Vector	Library Description
		mild lateral ventricular enlargement. For donor F, pathology indicated moderate Alzheimer's disease, recent multiple infarctions involving left thalamus, left parietal and occipital lobes (microscopic) and right cerebellum (gross), mild atherosclerosis involving middle cerebral arteries bilaterally and mild cerebral amyloid angiopathy. For donor G, pathology indicated severe Alzheimer's disease, mild atherosclerosis involving the middle cerebral and basilar arteries, and cerebral atrophy consistent with Alzheimer's disease. For donor D, patient history included Huntington's chorea. Donor E was taking nitroglycerin and dopamine; donor F was taking Lopressor, heparin, ceftriaxone, captopril, Isordil, nitroglycerin, Clinoril, Ecotrin and tacrine; and donor G was taking insulin.
OVARDIR01	PCDNA2.1	This random primed library was constructed using RNA isolated from right ovary tissue removed from a 45-year-old Caucasian female during total abdominal hysterectomy, bilateral salpingo-oophorectomy, vaginal suspension and fixation, and incidental appendectomy. Pathology indicated stromal hyperthecosis of the right and left ovaries. Pathology for the matched tumor tissue indicated a dermoid cyst (benign cystic teratoma) in the left ovary. Multiple (3) intramural leiomyomata were identified. The cervix showed squamous metaplasia. Patient history included metrorrhagia, female stress incontinence, alopecia, depressive disorder, pneumonia, normal delivery, and deficiency anemia. Family history included benign hypertension, atherosclerotic coronary artery disease, hyperlipidemia, and primary tuberculous complex.
OVARDIT01	pINCY	Library was constructed using RNA isolated from diseased ovary tissue removed from a 39-year-old Caucasian female during total abdominal hysterectomy, bilateral salpingo-oophorectomy, dilation and curettage, partial colectomy, incidental appendectomy, and temporary colostomy. Pathology indicated the right and left adnexa were extensively involved by endometriosis. Endometriosis also involved the anterior and posterior serosal surfaces of the uterus and the cul-de-sac and the mesentery and muscularis propria of the sigmoid colon. Pathology for the associated tumor tissue indicated multiple (3) intramural, 1 subserosal) leiomyomata. Family history included hyperlipidemia, benign hypertension, atherosclerotic coronary artery disease, depressive disorder, brain cancer, and type II diabetes.
PANCNOT07	pINCY	Library was constructed using RNA isolated from the pancreatic tissue of a Caucasian male fetus, who died at 23 weeks' gestation.
PROSTUS23	pINCY	This subtracted prostate tumor library was constructed using 10 million clones from a pooled prostate tumor library that was subjected to 2 rounds of subtractive hybridization with 10 million clones from a pooled prostate tissue library. The

Table 6 (cont.)

Library	Vector	Library Description
		starting library for subtraction was constructed by pooling equal numbers of clones from 4 prostate tumor libraries using mRNA isolated from prostate tumor removed from Caucasian males at ages 58 (A), 61 (B), 66 (C), and 68 (D) during prostatectomy with lymph node excision. Pathology indicated adenocarcinoma in all donors. History included elevated PSA, induration and tobacco abuse in donor A; elevated PSA, induration, prostate hyperplasia, renal failure, osteoarthritis, renal artery stenosis, benign HTN, thrombocytopenia, hyperlipidemia, tobacco/alcohol abuse and hepatitis C (carrier) in donor B; elevated PSA, induration, and tobacco abuse in donor C; and elevated PSA, induration, hypercholesterolemia, and kidney calculus in donor D. The hybridization probe for subtraction was constructed by pooling equal numbers of cDNA clones from 3 prostate tissue libraries derived from prostate tissue, prostate epithelial cells, and fibroblasts from prostate stroma from 3 different donors. Subtractive hybridization conditions were based on the methodologies of Swaroop et al., NAR 19 (1991):1954 and Bonaldo, et al. Genome Research 6 (1996):791.
SININOT05	pINCY	Library was constructed using RNA isolated from ileum tissue obtained from a 30-year-old Caucasian female during partial colectomy, open liver biopsy, incidental appendectomy, and permanent colostomy. Patient history included endometriosis. Family history included hyperlipidemia, anxiety, and upper lobe lung cancer, stomach cancer, liver cancer, and cirrhosis.
SINTBST01	pINCY	Library was constructed using RNA isolated from the ileum tissue of an 18-year-old Caucasian female. The ileum tissue, along with the cecum and appendix, were removed during bowel anastomosis. Pathology indicated Crohn's disease of the ileum, involving 15 cm of the small bowel. The cecum and appendix were unremarkable, and the margins were uninvolved. The patient presented with abdominal pain and regional enteritis. Patient history included osteoporosis of the vertebra and abnormal blood chemistry. Patient medications included Prilosec (omeprazole), Pentasa (mesalamine), amoxicillin, and multivitamins. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.
SINTNOR01	PCDNA2.1	This random primed library was constructed using RNA isolated from small intestine tissue removed from a 31-year-old Caucasian female during Roux-en-Y gastric bypass. Patient history included clinical obesity.
SINTNOT18	pINCY	Library was constructed using RNA isolated from small intestine tissue obtained from a 59-year-old male.
SINTTMR02	PCDNA2.1	This random primed library was constructed using RNA isolated from small intestine tissue removed from a 59-year-old male. Pathology for the matched tumor tissue

Table 6 (cont.)

Library	Vector	Library Description
TESTTUT03	pINCY	indicated multiple (9) carcinoid tumors, grade 1, in the small bowel. The largest tumor was associated with a large mesenteric mass. Multiple convoluted segments of bowel were adhered to the tumor. A single (1 of 13) regional lymph node was positive for malignancy. The peritoneal biopsy indicated focal fat necrosis. Library was constructed using RNA isolated from right testicular tumor tissue removed from a 45-year-old Caucasian male during a unilateral orchiectomy. Pathology indicated seminoma. Patient history included hyperlipidemia and stomach ulcer. Family history included cerebrovascular disease, skin cancer, hyperlipidemia, acute myocardial infarction, and atherosclerotic coronary artery disease.
THYRDIE01	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from diseased thyroid tissue removed from a 22-year-old Caucasian female during closed thyroid biopsy, partial thyroidectomy, and regional lymph node excision. Pathology indicated adenomatous hyperplasia. The patient presented with malignant neoplasm of the thyroid. Patient history included normal delivery, alcohol abuse, and tobacco abuse. Previous surgeries included myringotomy. Patient medications included an unspecified type of birth control pills. Family history included hyperlipidemia and depressive disorder in the mother; and benign hypertension, congestive heart failure, and chronic leukemia in the grandparent(s).
UTRSNOT11	pINCY	Library was constructed using RNA isolated from uterine myometrial tissue removed from a 43-year-old female during a vaginal hysterectomy and removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated that the myometrium contained an intramural and a submucosal leiomyoma. Family history included benign hypertension, hyperlipidemia, colon cancer, type II diabetes, and atherosclerotic coronary artery disease.

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1998) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less Signal peptide hits: Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score ≥ GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of
5 SEQ ID NO:1-32,
 - b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-32,
 - c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, and
10 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32.
2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-
15 32.
3. An isolated polynucleotide encoding a polypeptide of claim 1.
4. An isolated polynucleotide encoding a polypeptide of claim 2.
- 20 5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:33-64.
6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
25
7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
- 30 9. A method for producing a polypeptide of claim 1, the method comprising:
 - a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and
35 b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.

11. An isolated polynucleotide selected from the group consisting of:

- 5 of SEQ ID NO:33-64,
- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting
 - b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:33-64,
 - c) a polynucleotide complementary to a polynucleotide of a),
 - d) a polynucleotide complementary to a polynucleotide of b), and
 - 10 e) an RNA equivalent of a)-d).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 11.

15 13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization
- 20 complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

25 14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- 30 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

35

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-32.

18. A method for treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment the composition of claim 16.

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of functional TRICH, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

24. A method for treating a disease or condition associated with overexpression of functional TRICH, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim 1, said method comprising the steps of:

- a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

28. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

29. A diagnostic test for a condition or disease associated with the expression of TRICH in a biological sample comprising the steps of:

- 5 a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and
b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

30. The antibody of claim 10, wherein the antibody is:

- 10 a) a chimeric antibody,
b) a single chain antibody,
c) a Fab fragment,
d) a F(ab')₂ fragment, or
e) a humanized antibody.

15 31. A composition comprising an antibody of claim 10 and an acceptable excipient.

32. A method of diagnosing a condition or disease associated with the expression of TRICH in a subject, comprising administering to said subject an effective amount of the composition of claim 20 31.

33. A composition of claim 31, wherein the antibody is labeled.

34. A method of diagnosing a condition or disease associated with the expression of TRICH in a subject, comprising administering to said subject an effective amount of the composition of claim 25 33.

35. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 10 comprising:

- 30 a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, or an immunogenic fragment thereof, under conditions to elicit an antibody response;
b) isolating antibodies from said animal; and

c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32.

5 36. An antibody produced by a method of claim 35.

37. A composition comprising the antibody of claim 36 and a suitable carrier.

38. A method of making a monoclonal antibody with the specificity of the antibody of claim
10 10 comprising:

a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32, or an immunogenic fragment thereof, under conditions to elicit an antibody response;

b) isolating antibody producing cells from the animal;

15 c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells;

d) culturing the hybridoma cells; and

e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32.

20

39. A monoclonal antibody produced by a method of claim 38.

40. A composition comprising the antibody of claim 39 and a suitable carrier.

25 41. The antibody of claim 10, wherein the antibody is produced by screening a Fab expression library.

42. The antibody of claim 10, wherein the antibody is produced by screening a recombinant immunoglobulin library.

30

43. A method for detecting a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32 in a sample, comprising the steps of:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and

b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32 in the sample.

5 44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32 from a sample, the method comprising:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and

10 b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-32.

45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

15

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

20

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

25

52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

30

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.

58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.

5 59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.

60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.

10 61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.

62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.

63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.

15 64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.

65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.

20 66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.

67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:23.

68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:24.

25 69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:25.

70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:26.

30 71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:27.

72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:28.

73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:29.

74. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:30.
75. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:31.
- 5 76. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:32.
77. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:33.
- 10 78. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:34.
79. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:35.
- 15 80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:36.
81. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:37.
- 20 82. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:38.
83. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:39.
- 25 84. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:40.
- 30 85. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:41.

86. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:42.

87. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:43.

88. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:44.

89. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:45.

90. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:46.

91. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:47.

92. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:48.

93. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:49.

94. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:50.

95. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:51.

96. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:52.

97. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:53.

98. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:54.

99. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:55.

100. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:56.

101. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:57.

102. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:58.

103. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:59.

104. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:60.

105. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:61.

106. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:62.

107. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:63.

108. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:64.

<110> INCYTE GENOMICS, INC.
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 DAS, Debopriya
 POLICKY, Jennifer L.

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<130> PI-0149 PCT

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<151> 2000-07-07; 2000-07-14; 2000-07-21; 2000-07-28

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Ala	Tyr	Leu	Ala	Leu	Gly	Thr	Gly	Val	Phe	Trp	Thr	Leu	Glu	Gly
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Arg	Ala	Ala	Gln	Asp	Ser	Ser	Arg	Ser	Phe	Gln	Arg	Asp	Lys	Trp

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Glu	Leu	Leu	Gln	Asn	Phe	Thr	Cys	Leu	Asp	Arg	Pro	Ala	Leu	Asp
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Ser	Leu	Ile	Arg	Asp	Val	Val	Gln	Ala	Tyr	Lys	Asn	Gly	Ala	Ser
	80		85		90									
Leu	Leu	Ser	Asn	Thr	Thr	Ser	Met	Gly	Arg	Trp	Glu	Leu	Val	Gly
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Ser	Phe	Phe	Phe	Ser	Val	Ser	Thr	Ile	Thr	Thr	Ile	Gly	Tyr	Gly
	110		115		120									
Asn	Leu	Ser	Pro	Asn	Thr	Met	Ala	Ala	Arg	Leu	Phe	Cys	Ile	Phe
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Phe	Ala	Leu	Val	Gly	Ile	Pro	Leu	Asn	Leu	Val	Val	Leu	Asn	Arg
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Leu	Gly	Gly	Thr	Trp	Gln	Asp	Pro	Asp	Lys	Ala	Arg	Trp	Leu	Ala
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Gly	Ser	Gly	Ala	Leu	Leu	Ser	Gly	Leu	Leu	Leu	Phe	Leu	Leu	Leu
	185		190		195									
Pro	Pro	Leu	Leu	Phe	Ser	His	Met	Glu	Gly	Trp	Ser	Tyr	Thr	Glu
	200		205		210									
Gly	Phe	Tyr	Phe	Ala	Phe	Ile	Thr	Leu	Ser	Thr	Val	Gly	Phe	Gly
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Asp	Tyr	Val	Ile	Gly	Met	Asn	Pro	Ser	Gln	Arg	Tyr	Pro	Leu	Trp
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Tyr	Lys	Asn	Met	Val	Ser	Leu	Trp	Ile	Leu	Phe	Gly	Met	Ala	Trp
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Gly	Arg	Val	Cys	Ser	Cys	Cys	His	His	Ser	Ser	Lys	Glu	Asp	Phe
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Lys	Ser	Gln	Ser	Trp	Arg	Gln	Gly	Pro	Asp	Arg	Glu	Pro	Glu	Ser
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His	Ser	Pro	Gln	Gln	Gly	Cys	Tyr	Pro	Glu	Gly	Pro	Met	Gly	Ile
	305		310		315									
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Ser	Pro	Leu	Leu	Thr	Gly	Asp	Ser	Ser	Gly	Leu	Pro	Pro	Ala	Pro
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Ser	Ala	Pro	Thr	His	Gly	Val	Lys	Ala	Ser	Gly	Gly	Leu	Gly	Thr
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Ile	Leu	His	Pro	Gln	Asp	Pro	Asp	Lys	Ala	Arg	Trp	Leu	Ala	Gly
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Ser	Gly	Ala	Leu	Leu	Ser	Gly	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Pro
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Pro	Leu	Leu	Phe	Ser	His	Met	Glu	Gly	Trp	Ser	Tyr	Thr	Glu	Gly
				95					100					105
Phe	Tyr	Phe	Ala	Phe	Ile	Thr	Leu	Ser	Thr	Val	Gly	Phe	Gly	Asp
				110					115					120
Tyr	Val	Ile	Gly	Met	Asn	Pro	Ser	Gln	Arg	Tyr	Pro	Leu	Trp	Tyr

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Lys Asn Met Val	Ser Leu Trp Ile Leu	Phe Gly Met Ala Trp	Leu		
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Ala Leu Ile Ile	Lys Leu Ile Leu Ser	Gln Leu Glu Thr Pro	Gly		
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Arg Val Cys Ser	Cys Cys His His Ser	Ser Lys Glu Asp Phe	Lys		
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Ser Gln Ser Trp	Arg Gln Gly Pro Asp	Arg Glu Pro Glu Ser	His		
	185		190		195
Ser Pro Gln Gln	Gly Cys Tyr Pro Glu	Gly Pro Met Gly Ile	Ile		
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Glu Ala Gln Arg	Phe Ser His Leu Pro	Lys Arg Ser Ala Val	Asp
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Ile Glu Phe Val	Glu Leu Ser Tyr Ser	Val Arg Glu Gly Pro	Cys
	65	70	75
Trp Arg Lys Arg	Gly Tyr Lys Thr Leu	Leu Lys Cys Leu Ser	Gly
	80	85	90
Lys Phe Cys Arg	Arg Glu Leu Ile Gly	Ile Met Gly Pro Ser	Gly
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Ala Gly Lys Ser	Thr Phe Met Asn Ile	Leu Ala Gly Tyr Arg	Glu
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Val Thr Glu Ile	Leu Thr Ala Leu Gly	Leu Met Ser Cys Ser	His
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Thr Ile His Gln	Pro Ser Ala Lys Leu	Phe Glu Met Phe Asp	Lys
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Thr Asn Leu Ile	Pro Tyr Leu Lys Gly	Leu Gly Leu His Cys	Pro
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Gly Leu Cys Ala	Met Ala Glu Lys Lys	Ser Ser Pro Glu Lys	Asn		
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Glu Val Pro Ala	Pro Cys Pro Pro Cys	Pro Pro Glu Val Asp	Pro		
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Ile Leu Phe Lys	Arg Thr Phe Leu Ser	Ile Leu Arg Asp Thr	Val		
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Leu Thr His Leu	Arg Phe Met Ser His	Val Val Ile Gly Val	Leu		
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Ile Gly Leu Leu	Tyr Leu His Ile Gly	Asp Asp Ala Ser Lys	Val		
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Phe Asn Asn Thr	Gly Cys Leu Phe Phe	Ser Met Leu Phe Leu	Met		
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Phe Ala Ala Leu	Met Pro Thr Val Leu	Thr Val Pro Leu Glu	Met		
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Ala Val Phe Met	Arg Glu His Leu Asn	Tyr Trp Tyr Ser Leu	Lys		
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Ala Tyr Tyr Leu	Ala Lys Thr Met Ala	Asp Val Pro Phe Gln	Val		
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Val Cys Pro Val	Val Tyr Cys Ser Ile	Val Tyr Trp Met Thr	Gly		
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Gln Pro Ala Glu	Thr Ser Arg Phe Leu	Leu Phe Ser Ala Leu	Ala		
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Thr Ala Thr Ala	Leu Val Ala Gln Ser	Leu Gly Leu Leu Ile	Gly		
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Ala Ala Ser Asn	Ser Leu Gln Val Ala	Thr Phe Val Gly Pro	Val		
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Thr Ala Ile Pro	Val Leu Leu Phe Ser	Gly Phe Phe Val Ser	Phe		
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Lys Thr Ile Pro	Thr Tyr Leu Gln Trp	Ser Ser Tyr Leu Ser	Tyr		
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Val Arg Tyr Gly	Phe Glu Gly Val Ile	Leu Thr Ile Tyr Gly	Met		
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Glu Arg Gly Asp	Leu Thr Cys Leu Glu	Glu Arg Cys Pro Phe	Arg		
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Glu Pro Gln Ser	Ile Leu Arg Ala Leu	Asp Val Glu Asp Ala	Lys		
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Leu Tyr Met Asp	Phe Leu Val Leu Gly	Ile Phe Phe Leu Ala	Leu		
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Pro Val Asn Leu	Phe Glu Gln Phe	Gln Glu Val Ala	Asn Thr Tyr
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Phe Leu Phe Leu	Leu Ile Leu Gln	Leu Ile Pro Gln	Ile Ser Ser

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Ile	Ile	Lys	Leu	Glu	Asn	Asn	Gln	Phe	Val	Ala	Ala	Asp	Leu	Leu
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Pro	Val	Thr	Ser	Glu	Leu	Gly	Asp	Ile	Ser	Lys	Leu	Ala	Lys	Phe
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Asp	Gly	Glu	Val	Ile	Cys	Glu	Pro	Pro	Asn	Asn	Lys	Leu	Asp	Lys
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Phe	Ser	Gly	Thr	Leu	Tyr	Trp	Lys	Glu	Asn	Lys	Phe	Pro	Leu	Ser
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Glu	Gly	Ala	Leu	Val	Thr	Ala	Ala	Arg	Asn	Phe	Gly	Phe	Val	Phe
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Arg	Ser	Arg	Thr	Pro	Lys	Thr	Ile	Thr	Val	His	Glu	Met	Gly	Thr
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Ala	Ile	Thr	Tyr	Gln	Leu	Leu	Ala	Ile	Leu	Asp	Phe	Asn	Asn	Ile
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Val	Leu	Glu	Val	Arg	Glu	Glu	Leu	Arg	Lys	Ala	Arg	Glu	Lys	Met
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Leu	Glu	Ala	Asp	Met	Glu	Leu	Glu	Phe	Leu	Glu	Thr	Ala	Cys	Ala
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Cys	Lys	Ala	Val	Ile	Cys	Cys	Arg	Val	Thr	Pro	Leu	Gln	Lys	Ala
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Gln	Val	Val	Glu	Leu	Val	Lys	Lys	Tyr	Lys	Lys	Ala	Val	Thr	Leu
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Ala	Ile	Gly	Asp	Gly	Ala	Asn	Asp	Val	Ser	Met	Ile	Lys	Thr	Ala
				815					820					825
His	Ile	Gly	Val	Gly	Ile	Ser	Gly	Gln	Glu	Gly	Ile	Gln	Ala	Val
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Leu	Ala	Ser	Asp	Tyr	Ser	Phe	Ser	Gln	Phe	Lys	Phe	Leu	Gln	Arg
				845					850					855
Leu	Leu	Leu	Val	His	Gly	Arg	Trp	Ser	Tyr	Leu	Arg	Met	Cys	Lys
				860					865					870
Phe	Leu	Cys	Tyr	Phe	Phe	Tyr	Lys	Asn	Phe	Ala	Phe	Thr	Met	Val
				875					880					885
His	Phe	Trp	Phe	Gly	Phe	Phe	Cys	Gly	Phe	Ser	Ala	Gln	Thr	Val
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Gln	Arg	Ser	Met	Glu	Tyr	Pro	Lys	Leu	Tyr	Glu	Pro	Gly	Gln	Leu
				935					940					945
Asn	Leu	Leu	Phe	Asn	Lys	Arg	Glu	Phe	Phe	Ile	Cys	Ile	Ala	Gln
				950					955					960
Gly	Ile	Tyr	Thr	Ser	Val	Leu	Met	Phe	Phe	Ile	Pro	Tyr	Gly	Val
				965					970					975
Phe	Ala	Asp	Ala	Thr	Arg	Asp	Asp	Gly	Thr	Gln	Leu	Ala	Asp	Tyr
				980					985					990
Gln	Ser	Phe	Ala	Val	Thr	Val	Ala	Thr	Ser	Leu	Val	Ile	Val	Val
				995					1000					1005
Ser	Val	Gln	Ile	Gly	Leu	Asp	Thr	Gly	Tyr	Trp	Thr	Ala	Ile	Asn
				1010					1015					1020
His	Phe	Phe	Ile	Trp	Gly	Ser	Leu	Ala	Val	Tyr	Phe	Ala	Ile	Leu
				1025					1030					1035
Phe	Ala	Met	His	Ser	Asn	Gly	Leu	Phe	Asp	Met	Phe	Pro	Asn	Gln
				1040					1045					1050
Phe	Arg	Phe	Val	Gly	Asn	Ala	Gln	Asn	Thr	Leu	Ala	Gln	Pro	Thr
				1055					1060					1065
Val	Trp	Leu	Thr	Ile	Val	Leu	Thr	Thr	Val	Val	Cys	Ile	Met	Pro

	1070		1075		1080
Val	Val	Ala	Phe	Arg	Phe
	1085		1090		1095
Ser	Asp	Thr	Val	Arg	Tyr
	1100		1105		1110
Ala	Gln	His	Arg	Cys	Met
	1115		1120		1125
Arg	Ser	Gly	Tyr	Ala	Phe
	1130		1135		1140
Ile	Met	Ser	Gly	Lys	Asn
	1145		1150		1155
Ser	Phe	Thr	Thr	Arg	Ser
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Arg	Lys	Lys	Ser	Asp	Ser
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Val	Glu
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Met	Thr
	110
Phe	Pro
	125
Thr	Arg
	140
Arg	Ser
	155
Val	His
	170
Ser	Ala
	185
Gln	Asn
	200
Asp	Leu
	215
Glu	Glu
	230
Ala	Ser
	245
Arg	Leu
	260
Val	Leu
	275
Trp	Val

Leu	Ala	Phe	Gln	Leu	Val	Ser	Phe	Thr	Tyr	Ile	Trp	Ile
5	10	15	20	25	30	35	40	45	50	55	60	65
Val	Cys	Ala	Ala	Ser	Asn	Ile	Lys	Met	Thr	His	Gln	Glu
20	25	30	35	40	45	50	55	60	65	70	75	80
Ser	Ser	Met	Lys	Gln	Thr	Cys	Lys	Gln	Lys	Asp	Asp	Ser
35	40	45	50	55	60	65	70	75	80	85	90	95
Thr	Arg	Met	Lys	Lys	Asp	Asp	Ser	Thr	Lys	Ala	Arg	Pro
50	55	60	65	70	75	80	85	90	95	100	105	110
Leu	Leu	His	Ile	Glu	Asp	Asn	Asp	Phe	Ala	Met	Arg	Thr
65	70	75	80	85	90	95	100	105	110	115	120	125
Ser	Pro	Val	Pro	Val	Gly	Ile	Asp	Val	His	Pro	Gly	Val
80	85	90	95	100	105	110	115	120	125	130	135	140
Gly	Ser	Pro	Val	Pro	Val	Gly	Ile	Asp	Val	His	Pro	Gly
80	85	90	95	100	105	110	115	120	125	130	135	140
Val	Glu	Ser	Ile	Asp	Ser	Ile	Ser	Glu	Thr	Asn	Met	Asp
95	100	105	110	115	120	125	130	135	140	145	150	155
Asp	Ser	Ile	Asp	Ser	Ile	Ser	Glu	Thr	Asn	Met	Asp	Ser
110	115	120	125	130	135	140	145	150	155	160	165	170
Leu	Arg	His	Tyr	Trp	Lys	Asp	Glu	Arg	Leu	Ser	Thr	Val
110	115	120	125	130	135	140	145	150	155	160	165	170
Thr	Arg	Lys	Ile	Trp	Val	Pro	Asp	Ile	Phe	Phe	Val	His
125	130	135	140	145	150	155	160	165	170	175	180	185
Val	Pro	Ser	Thr	Ala	Asn	Lys	Ser	Met	Thr	Phe	Asp	His
125	130	135	140	145	150	155	160	165	170	175	180	185
Arg	Ser	Phe	Ile	His	Asp	Thr	Thr	Met	Glu	Asn	Ile	Met
140	145	150	155	160	165	170	175	180	185	190	195	200
Leu	Arg	Met	Leu	Asn	Ile	Met	Leu	Arg	Ile	Thr	Val	Ser
155	160	165	170	175	180	185	190	195	200	205	210	215
Val	His	Pro	Asp	Gly	Asn	Val	Leu	Leu	Ser	Leu	Arg	Ile
170	175	180	185	190	195	200	205	210	215	220	225	230
Ser	Ala	Met	Cys	Phe	Met	Asp	Phe	Ser	Arg	Phe	Pro	Leu
185	190	195	200	205	210	215	220	225	230	235	240	245
Gln	Asn	Cys	Ser	Leu	Glu	Leu	Glu	Ser	Tyr	Ala	Tyr	Asn
200	205	210	215	220	225	230	235	240	245	250	255	260
Asp	Leu	Met	Leu	Tyr	Trp	Lys	His	Gly	Asn	Lys	Ser	Leu
215	220	225	230	235	240	245	250	255	260	265	270	275
Thr	Arg	Glu	His	Met	Ser	Leu	Ser	Gln	Phe	Ile	Glu	Asp
225	230	235	240	245	250	255	260	265	270	275	280	285
Ser	Glu	Glu	His	Met	Ser	Leu	Ser	Gln	Phe	Ile	Glu	Asp
230	235	240	245	250	255	260	265	270	275	280	285	290
Ala	Ser	Ser	Gly	Leu	Ala	Phe	Tyr	Ser	Ser	Thr	Gly	Trp
245	250	255	260	265	270	275	280	285	290	295	300	305
Trp	Val	Ser	Phe	Trp	Ile	Asp	Arg	Arg	Ala	Val	Pro	Ala
255	260	265	270	275	280	285	290	295	300	305	310	315
Arg	Leu	Phe	Ile	Ile	Ser	Val	Leu	Arg	Arg	His	Val	Phe
260	265	270	275	280	285	290	295	300	305	310	315	320
Val	Leu	Pro	Thr	Tyr	Tyr	Pro	Ala	Ile	Leu	Met	Val	Met
275	280	285	290	295	300	305	310	315	320	325	330	335
Leu	Arg	Val	Pro	Ala	Arg	Val	Pro	Ala	Arg	Val	Pro	Ala
285	290	295	300	305	310	315	320	325	330	335	340	345

	290		295		300
Ser Leu Gly Ile	Thr Thr Val Leu Thr	Met Ser Thr Ile Ile	Thr		
	305		310		315
Ala Val Ser Ala	Ser Met Pro Gln Val	Ser Tyr Leu Lys Ala	Val		
	320		325		330
Asp Val Tyr Leu	Trp Val Ser Ser Leu	Phe Val Phe Leu Ser	Val		
	335		340		345
Ile Glu Tyr Ala	Ala Val Asn Tyr Leu	Thr Thr Val Glu Glu	Arg		
	350		355		360
Lys Gln Phe Lys	Lys Thr Gly Lys Ile	Ser Arg Met Tyr Asn	Ile		
	365		370		375
Asp Ala Val Gln	Ala Met Ala Phe Asp	Gly Cys Tyr His Asp	Ser		
	380		385		390
Glu Ile Asp Met	Asp Gln Thr Ser Leu	Ser Leu Asn Ser Glu	Asp		
	395		400		405
Phe Met Arg Arg	Lys Ser Ile Cys Ser	Pro Ser Thr Asp Ser	Ser		
	410		415		420
Arg Ile Lys Arg	Arg Lys Ser Leu Gly	Gly His Val Gly Arg	Ile		
	425		430		435
Ile Leu Glu Asn	Asn His Val Ile Asp	Thr Tyr Ser Arg Ile	Leu		
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Phe Pro Ile Val	Tyr Ile Leu Phe Asn	Leu Phe Tyr Trp Gly	Val		
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Tyr Val					

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	20	25	30
Ile Ala Asn Ala	Arg Val Gln Asn Cys	Ala Ile Ile Tyr Cys	Asn
	35	40	45
Asp Gly Phe Cys	Glu Met Thr Gly Phe	Ser Arg Pro Asp Val	Met
	50	55	60
Gln Lys Pro Cys	Thr Cys Asp Phe Leu	His Gly Pro Glu Thr	Lys
	65	70	75
Arg His Asp Ile	Ala Gln Ile Ala Gln	Ala Leu Leu Gly Ser	Glu
	80	85	90
Glu Arg Lys Val	Glu Val Thr Tyr Tyr	His Lys Asn Gly Ser	Thr
	95	100	105
Phe Ile Cys Asn	Thr His Ile Ile Pro	Val Lys Asn Gln Glu	Gly
	110	115	120
Val Ala Met Met	Phe Ile Ile Asn Phe	Glu Tyr Val Thr Asp	Asn
	125	130	135
Glu Asn Ala Ala	Thr Pro Glu Arg Val	Asn Pro Ile Leu Pro	Ile
	140	145	150
Lys Thr Val Asn	Arg Lys Phe Phe Gly	Phe Lys Phe Pro Gly	Leu
	155	160	165
Arg Val Leu Thr	Tyr Arg Lys Gln Ser	Leu Pro Gln Glu Asp	Pro
	170	175	180
Asp Val Val Val	Ile Asp Ser Ser Lys	His Ser Asp Asp Ser	Val
	185	190	195
Ala Met Lys His	Phe Lys Ser Pro Thr	Lys Glu Ser Cys Ser	Pro
	200	205	210
Ser Glu Ala Asp	Asp Thr Lys Ala Leu	Ile Gln Pro Ser Lys	Cys
	215	220	225
Ser Pro Leu Val	Asn Ile Ser Gly Pro	Leu Asp His Ser Ser	Pro

	230		235		240
Lys Arg Gln Trp	Asp Arg Leu Tyr Pro	Asp Met Leu Gln Ser	Ser		
	245		250		255
Ser Gln Leu Ser	His Ser Arg Ser Arg	Glu Ser Leu Cys Ser	Ile		
	260		265		270
Arg Arg Ala Ser	Ser Val His Asp Ile	Glu Gly Phe Gly Val	His		
	275		280		285
Pro Lys Asn Ile	Phe Arg Asp Arg His	Ala Ser Glu Asp Asn	Gly		
	290		295		300
Arg Asn Val Lys	Gly Pro Phe Asn His	Ile Lys Ser Ser Leu	Leu		
	305		310		315
Gly Ser Thr Ser	Asp Ser Asn Leu Asn	Lys Tyr Ser Thr Ile	Asn		
	320		325		330
Lys Ile Pro Gln	Leu Thr Leu Asn Phe	Ser Glu Val Lys Thr	Glu		
	335		340		345
Lys Lys Asn Ser	Ser Pro Pro Ser Ser	Asp Lys Thr Ile Ile	Ala		
	350		355		360
Pro Lys Val Lys	Asp Arg Thr His Asn	Val Thr Glu Lys Val	Thr		
	365		370		375
Gln Val Leu Ser	Leu Gly Ala Asp Val	Leu Pro Glu Tyr Lys	Leu		
	380		385		390
Gln Thr Pro Arg	Ile Asn Lys Phe Thr	Ile Leu His Tyr Ser	Pro		
	395		400		405
Phe Lys Ala Val	Trp Asp Trp Leu Ile	Leu Leu Leu Val Ile	Tyr		
	410		415		420
Thr Ala Ile Phe	Thr Pro Tyr Ser Ala	Ala Phe Leu Leu Asn	Asp		
	425		430		435
Arg Glu Glu Gln	Lys Arg Arg Glu Cys	Gly Tyr Ser Cys Ser	Pro		
	440		445		450
Leu Asn Val Val	Asp Leu Ile Val Asp	Ile Met Phe Ile Ile	Asp		
	455		460		465
Ile Leu Ile Asn	Phe Arg Thr Thr Tyr	Val Asn Gln Asn Glu	Glu		
	470		475		480
Val Val Ser Asp	Pro Ala Lys Ile Ala	Ile His Tyr Phe Lys	Gly		
	485		490		495
Trp Phe Leu Ile	Asp Met Val Ala Ala	Ile Pro Phe Asp Leu	Leu		
	500		505		510
Ile Phe Gly Ser	Gly Ser Asp Glu Thr	Thr Thr Leu Ile Gly	Leu		
	515		520		525
Leu Lys Thr Ala	Arg Leu Leu Arg Leu	Val Arg Val Ala Arg	Lys		
	530		535		540
Leu Asp Arg Tyr	Ser Glu Tyr Gly Ala	Ala Val Leu Met Leu	Leu		
	545		550		555
Met Cys Ile Phe	Ala Leu Ile Ala His	Trp Leu Ala Cys Ile	Trp		
	560		565		570
Tyr Ala Ile Gly	Asn Val Glu Arg Pro	Tyr Leu Thr Asp Lys	Ile		
	575		580		585
Gly Trp Leu Asp	Ser Leu Gly Gln Gln	Ile Gly Lys Arg Tyr	Asn		
	590		595		600
Asp Ser Asp Ser	Ser Ser Gly Pro Ser	Ile Lys Asp Lys Tyr	Val		
	605		610		615
Thr Ala Leu Tyr	Phe Thr Phe Ser Ser	Leu Thr Ser Val Gly	Phe		
	620		625		630
Gly Asn Val Ser	Pro Asn Thr Asn Ser	Glu Lys Ile Phe Ser	Ile		
	635		640		645
Cys Val Met Leu	Ile Gly Ser Leu Met	Tyr Ala Ser Ile Phe	Gly		
	650		655		660
Asn Val Ser Ala	Ile Ile Gln Arg Leu	Tyr Ser Gly Thr Ala	Arg		
	665		670		675
Tyr His Met Gln	Met Leu Arg Val Lys	Glu Phe Ile Arg Phe	His		
	680		685		690
Gln Ile Pro Asn	Pro Leu Arg Gln Arg	Leu Glu Glu Tyr Phe	Gln		
	695		700		705
His Ala Trp Thr	Tyr Thr Asn Gly Ile	Asp Met Asn Met Val	Leu		
	710		715		720
Lys Gly Phe Pro	Glu Cys Leu Gln Ala	Asp Ile Cys Leu His	Leu		
	725		730		735

Asn	Gln	Thr	Leu	Leu	Gln	Asn	Cys	Lys	Ala	Phe	Arg	Gly	Ala	Ser
				740					745					750
Lys	Gly	Cys	Leu	Arg	Ala	Leu	Ala	Met	Lys	Phe	Lys	Thr	Thr	His
				755					760					765
Ala	Pro	Pro	Gly	Asp	Thr	Leu	Val	His	Cys	Gly	Asp	Val	Leu	Thr
				770					775					780
Ala	Leu	Tyr	Phe	Leu	Ser	Arg	Gly	Ser	Ile	Glu	Ile	Leu	Lys	Asp
				785					790					795
Asp	Ile	Val	Val	Ala	Ile	Leu	Gly	Lys	Asn	Asp	Ile	Phe	Gly	Glu
				800					805					810
Met	Val	His	Leu	Tyr	Ala	Lys	Pro	Gly	Lys	Ser	Asn	Ala	Asp	Val
				815					820					825
Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	Ile	Gln	Arg	Glu	Asp
				830					835					840
Leu	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Glu	Phe	Ser	Asp	His	Phe
				845					850					855
Leu	Thr	Asn	Leu	Glu	Leu	Thr	Phe	Asn	Leu	Arg	His	Glu	Ser	Ala
				860					865					870
Lys	Ala	Asp	Leu	Leu	Arg	Ser	Gln	Ser	Met	Asn	Asp	Ser	Glu	Gly
				875					880					885
Asp	Asn	Cys	Lys	Leu	Arg	Arg	Arg	Lys	Leu	Ser	Phe	Glu	Ser	Glu
				890					895					900
Gly	Glu	Lys	Glu	Asn	Ser	Thr	Asn	Asp	Pro	Glu	Asp	Ser	Ala	Asp
				905					910					915
Thr	Ile	Arg	His	Tyr	Gln	Ser	Ser	Lys	Arg	His	Phe	Glu	Glu	Lys
				920					925					930
Lys	Ser	Arg	Ser	Ser	Ser	Phe	Ile	Ser	Ser	Ile	Asp	Asp	Glu	Gln
				935					940					945
Lys	Pro	Leu	Phe	Ser	Gly	Ile	Val	Asp	Ser	Ser	Pro	Gly	Ile	Gly
				950					955					960
Lys	Ala	Ser	Gly	Leu	Asp	Phe	Glu	Glu	Thr	Val	Pro	Thr	Ser	Gly
				965					970					975
Arg	Met	His	Ile	Asp	Lys	Arg	Ser	His	Ser	Cys	Lys	Asp	Ile	Thr
				980					985					990
Asp	Met	Arg	Ser	Trp	Glu	Arg	Glu	Asn	Ala	His	Pro	Gln	Pro	Glu
				995					1000					1005
Asp	Ser	Ser	Pro	Ser	Ala	Leu	Gln	Arg	Ala	Ala	Trp	Gly	Ile	Ser
				1010					1015					1020
Glu	Thr	Glu	Ser	Asp	Leu	Thr	Tyr	Gly	Glu	Val	Glu	Gln	Arg	Leu
				1025					1030					1035
Asp	Leu	Leu	Gln	Glu	Gln	Leu	Asn	Arg	Leu	Glu	Ser	Gln	Met	Thr
				1040					1045					1050
Thr	Asp	Ile	Gln	Thr	Ile	Leu	Gln	Leu	Leu	Gln	Lys	Gln	Thr	Thr
				1055					1060					1065
Val	Val	Pro	Pro	Ala	Tyr	Ser	Met	Val	Thr	Ala	Gly	Ser	Glu	Tyr
				1070					1075					1080
Gln	Arg	Pro	Ile	Ile	Gln	Leu	Met	Arg	Thr	Ser	Gln	Pro	Glu	Ala
				1085					1090					1095
Ser	Ile	Lys	Thr	Asp	Arg	Ser	Phe	Ser	Pro	Ser	Ser	Gln	Cys	Pro
				1100					1105					1110
Glu	Phe	Leu	Asp	Leu	Glu	Lys	Ser	Lys	Leu	Lys	Ser	Lys	Glu	Ser
				1115					1120					1125
Leu	Ser	Ser	Gly	Val	His	Leu	Asn	Thr	Ala	Ser	Glu	Asp	Asn	Leu
				1130					1135					1140
Thr	Ser	Leu	Leu	Lys	Gln	Asp	Ser	Asp	Leu	Ser	Leu	Glu	Leu	His
				1145					1150					1155
Leu	Arg	Gln	Arg	Lys	Thr	Tyr	Val	His	Pro	Ile	Arg	His	Pro	Ser
				1160					1165					1170
Leu	Pro	Asp	Ser	Ser	Leu	Ser	Thr	Val	Gly	Ile	Val	Gly	Leu	His
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Arg	His	Val	Ser	Asp	Pro	Gly	Leu	Pro	Gly	Lys				
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Glu	Gly	Arg	Leu	Gln	Pro	Thr	Leu	Leu	Leu	Ala	Thr	Leu	Ser	Ala
				20					25					30
Ala	Phe	Gly	Ser	Ala	Phe	Gln	Tyr	Gly	Tyr	Asn	Leu	Ser	Val	Val
				35					40					45
Asn	Thr	Pro	His	Lys	Val	Phe	Lys	Ser	Phe	Tyr	Asn	Glu	Thr	Tyr
				50					55					60
Phe	Glu	Arg	His	Ala	Thr	Phe	Met	Asp	Gly	Lys	Leu	Met	Leu	Leu
				65					70					75
Leu	Trp	Ser	Cys	Thr	Val	Ser	Met	Phe	Pro	Leu	Gly	Gly	Leu	Leu
				80					85					90
Gly	Ser	Leu	Leu	Val	Gly	Leu	Leu	Val	Asp	Ser	Cys	Gly	Arg	Lys
				95					100					105
Gly	Thr	Leu	Leu	Ile	Asn	Asn	Ile	Phe	Ala	Ile	Ile	Pro	Ala	Ile
				110					115					120
Leu	Met	Gly	Val	Ser	Lys	Val	Ala	Lys	Ala	Phe	Glu	Leu	Ile	Val
				125					130					135
Phe	Ser	Arg	Val	Val	Leu	Gly	Val	Cys	Ala	Gly	Ile	Ser	Tyr	Ser
				140					145					150
Ala	Leu	Pro	Met	Tyr	Leu	Gly	Glu	Leu	Ala	Pro	Lys	Asn	Leu	Arg
				155					160					165
Gly	Met	Val	Gly	Thr	Met	Thr	Glu	Val	Phe	Val	Ile	Val	Gly	Val
				170					175					180
Phe	Leu	Ala	Gln	Ile	Phe	Ser	Leu	Gln	Ala	Ile	Leu	Gly	Asn	Pro
				185					190					195
Ala	Gly	Trp	Pro	Val	Leu	Leu	Ala	Leu	Thr	Gly	Val	Pro	Ala	Leu
				200					205					210
Leu	Gln	Leu	Leu	Thr	Leu	Pro	Phe	Phe	Pro	Glu	Ser	Pro	Arg	Tyr
				215					220					225
Ser	Leu	Ile	Gln	Lys	Gly	Asp	Glu	Ala	Thr	Ala	Arg	Gln	Ala	Leu
				230					235					240
Arg	Arg	Leu	Arg	Gly	His	Thr	Asp	Met	Glu	Ala	Glu	Leu	Glu	Asp
				245					250					255
Met	Arg	Ala	Glu	Ala	Arg	Ala	Glu	Arg	Ala	Glu	Gly	His	Leu	Ser
				260					265					270
Val	Leu	His	Leu	Cys	Ala	Leu	Arg	Ser	Leu	Arg	Trp	Gln	Leu	Leu
				275					280					285
Ser	Ile	Ile	Val	Leu	Met	Ala	Gly	Gln	Gln	Leu	Ser	Gly	Ile	Asn
				290					295					300
Ala	Ile	Asn	Tyr	Tyr	Ala	Asp	Thr	Ile	Tyr	Thr	Ser	Ala	Gly	Val
				305					310					315
Glu	Ala	Ala	His	Ser	Gln	Tyr	Val	Thr	Val	Gly	Ser	Gly	Val	Val
				320					325					330
Asn	Ile	Val	Met	Thr	Ile	Thr	Ser	Ala	Val	Leu	Val	Glu	Arg	Leu
				335					340					345
Gly	Arg	Arg	His	Leu	Leu	Leu	Ala	Gly	Tyr	Gly	Ile	Cys	Gly	Ser
				350					355					360
Ala	Cys	Leu	Val	Leu	Thr	Val	Val	Leu	Leu	Phe	Gln	Asn	Arg	Val
				365					370					375
Pro	Glu	Leu	Ser	Tyr	Leu	Gly	Ile	Ile	Cys	Val	Phe	Ala	Tyr	Ile
				380					385					390
Ala	Gly	His	Ser	Ile	Gly	Pro	Ser	Pro	Val	Pro	Ser	Val	Val	Arg
				395					400					405
Thr	Glu	Ile	Phe	Leu	Gln	Ser	Ser	Arg	Arg	Ala	Ala	Phe	Met	Val
				410					415					420
Asp	Gly	Ala	Val	His	Trp	Leu	Thr	Asn	Phe	Ile	Ile	Gly	Phe	Leu
				425					430					435
Phe	Pro	Ser	Ile	Gln	Glu	Ala	Ile	Gly	Ala	Tyr	Ser	Phe	Ile	Ile
				440					445					450
Phe	Ala	Gly	Ile	Cys	Leu	Leu	Thr	Ala	Ile	Tyr	Ile	Tyr	Val	Val
				455					460					465

Ile	Pro	Glu	Thr	Lys	Gly	Lys	Thr	Phe	Val	Glu	Ile	Asn	Arg	Ile
				470					475					480
Phe	Ala	Lys	Arg	Asn	Arg	Val	Lys	Leu	Pro	Glu	Glu	Lys	Glu	Glu
				485					490					495
Thr	Ile	Asp	Ala	Gly	Pro	Pro	Thr	Ala	Ser	Pro	Ala	Lys	Glu	Thr
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Ser	Phe													

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Ala	Pro	Ala	Ala	Gly	Gly	Leu	Asn	Ala	Gly	Pro	Val	Pro	Pro	Ala
				20					25					30
Ala	Met	Ser	Thr	Gln	Arg	Leu	Arg	Asn	Glu	Asp	Tyr	His	Asp	Tyr
				35					40					45
Ser	Ser	Thr	Asp	Val	Ser	Pro	Glu	Glu	Ser	Pro	Ser	Glu	Gly	Leu
				50					55					60
Asn	Asn	Leu	Ser	Ser	Pro	Gly	Ser	Tyr	Gln	Arg	Phe	Gly	Gln	Ser
				65					70					75
Asn	Ser	Thr	Thr	Trp	Phe	Gln	Thr	Leu	Ile	His	Leu	Leu	Lys	Gly
				80					85					90
Asn	Ile	Gly	Thr	Gly	Leu	Leu	Gly	Leu	Pro	Leu	Ala	Val	Lys	Asn
				95					100					105
Ala	Gly	Ile	Val	Met	Gly	Pro	Ile	Ser	Leu	Leu	Ile	Ile	Gly	Ile
				110					115					120
Val	Ala	Val	His	Cys	Met	Gly	Ile	Leu	Val	Lys	Cys	Ala	His	His
				125					130					135
Phe	Cys	Arg	Arg	Leu	Asn	Lys	Ser	Phe	Val	Asp	Tyr	Gly	Asp	Thr
				140					145					150
Val	Met	Tyr	Gly	Leu	Glu	Ser	Ser	Pro	Cys	Ser	Trp	Leu	Arg	Asn
				155					160					165
His	Ala	His	Trp	Gly	Arg	Arg	Val	Val	Asp	Phe	Phe	Leu	Ile	Val
				170					175					180
Thr	Gln	Leu	Gly	Phe	Cys	Cys	Val	Tyr	Phe	Val	Phe	Leu	Ala	Asp
				185					190					195
Asn	Phe	Lys	Gln	Val	Ile	Glu	Ala	Ala	Asn	Gly	Thr	Thr	Asn	Asn
				200					205					210
Cys	His	Asn	Asn	Glu	Thr	Val	Ile	Leu	Thr	Pro	Thr	Met	Asp	Ser
				215					220					225
Arg	Leu	Tyr	Met	Leu	Ser	Phe	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val
				230					235					240
Phe	Ile	Arg	Asn	Leu	Arg	Ala	Leu	Ser	Ile	Phe	Ser	Leu	Leu	Ala
				245					250					255
Asn	Ile	Thr	Met	Leu	Val	Ser	Leu	Val	Met	Ile	Tyr	Gln	Phe	Ile
				260					265					270
Val	Gln	Arg	Ile	Pro	Asp	Pro	Ser	His	Leu	Pro	Leu	Val	Ala	Pro
				275					280					285
Trp	Lys	Thr	Tyr	Pro	Leu	Phe	Phe	Gly	Thr	Ala	Ile	Phe	Ser	Phe
				290					295					300
Glu	Gly	Ile	Gly	Met	Val	Leu	Pro	Leu	Glu	Asn	Lys	Met	Lys	Asp
				305					310					315
Pro	Arg	Lys	Phe	Pro	Leu	Ile	Leu	Tyr	Leu	Gly	Met	Val	Ile	Val
				320					325					330
Thr	Ile	Leu	Tyr	Ile	Ser	Leu	Gly	Cys	Leu	Gly	Tyr	Leu	Gln	Phe
				335					340					345
Gly	Ala	Asn	Ile	Gln	Gly	Ser	Ile	Thr	Leu	Asn	Leu	Pro	Asn	Cys
				350					355					360

Trp	Leu	Tyr	Gln	Ser	Val	Lys	Leu	Leu	Tyr	Ser	Ile	Gly	Ile	Phe	
				365					370					375	
Phe	Thr	Tyr	Ala	Leu	Gln	Phe	Tyr	Val	Pro	Ala	Glu	Ile	Ile	Ile	
				380					385					390	
Pro	Phe	Phe	Val	Ser	Arg	Ala	Pro	Glu	Pro	Cys	Glu	Leu	Val	Val	
				395					400					405	
Asp	Leu	Phe	Val	Arg	Pro	Val	Leu	Val	Cys	Leu	Thr	Ser	Leu	Ser	
				410					415					420	
Gly	Ser	Val	Asp	Asn	Gly	Trp	Tyr	Gly	Thr	Glu	Ala	Asp	Gly	Thr	
				425					430					435	
Ser	Cys	Gly	Ser	Ala	Pro	Leu	Val	Phe	Val	Ser	Ser	Ser	Phe	Leu	
				440					445					450	
Ala	His	Pro	Trp	Leu	Ser	Phe	Arg	Cys	Glu	Ser	Gln	Trp	Val	Ser	
				455					460					465	
Cys	His	Arg	Asp	Thr	Val	Val	Val	Trp	Gly	Phe	Ala	Arg	Gly	Ile	
				470					475					480	
Leu	Ala	Ile	Leu	Ile	Pro	Arg	Leu	Asp	Leu	Val	Ile	Ser	Leu	Val	
				485					490					495	
Gly	Ser	Val	Ser	Ser	Ser	Ala	Leu	Ala	Leu	Ile	Ile	Pro	Pro	Leu	
				500					505					510	
Leu	Glu	Val	Thr	Thr	Phe	Tyr	Ser	Glu	Gly	Met	Ser	Pro	Leu	Thr	
				515					520					525	
Ile	Phe	Lys	Asp	Ala	Leu	Ile	Ser	Ile	Leu	Gly	Phe	Val	Gly	Phe	
				530					535					540	
Val	Val	Gly	Thr	Tyr	Glu	Ala	Leu	Tyr	Glu	Leu	Ile	Gln	Pro	Ser	
				545					550					555	
Asn	Ala	Pro	Ile	Phe	Ile	Asn	Ser	Thr	Cys	Ala	Phe	Ile			
				560					565						

<210> 9

<211> 958

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477898CD1

<400> 9

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1				5					10					15	
Asp	Thr	Ile	Ile	Arg	Lys	Phe	Glu	Gly	Gln	Ser	Arg	Lys	Phe	Leu	
				20					25					30	
Ile	Ala	Asn	Ala	Gln	Met	Glu	Asn	Cys	Ala	Ile	Ile	Tyr	Cys	Asn	
				35					40					45	
Asp	Gly	Phe	Cys	Glu	Leu	Phe	Gly	Tyr	Ser	Arg	Val	Glu	Val	Met	
				50					55					60	
Gln	Gln	Pro	Cys	Thr	Cys	Asp	Phe	Leu	Thr	Gly	Pro	Asn	Thr	Pro	
				65					70					75	
Ser	Ser	Ala	Val	Ser	Arg	Leu	Ala	Gln	Ala	Leu	Leu	Gly	Ala	Glu	
				80					85					90	
Glu	Cys	Lys	Val	Asp	Ile	Leu	Tyr	Tyr	Arg	Lys	Asp	Ala	Ser	Ser	
				95					100					105	
Phe	Arg	Cys	Leu	Val	Asp	Val	Val	Pro	Val	Lys	Asn	Glu	Asp	Gly	
				110					115					120	
Ala	Val	Ile	Met	Phe	Ile	Leu	Asn	Phe	Glu	Asp	Leu	Ala	Gln	Leu	
				125					130					135	
Leu	Ala	Lys	Cys	Ser	Ser	Arg	Ser	Leu	Ser	Gln	Arg	Leu	Leu	Ser	
				140					145					150	
Gln	Ser	Phe	Leu	Gly	Ser	Glu	Gly	Ser	His	Gly	Arg	Pro	Gly	Gly	
				155					160					165	
Pro	Gly	Pro	Gly	Thr	Gly	Arg	Gly	Lys	Tyr	Arg	Thr	Ile	Ser	Gln	
				170					175					180	
Ile	Pro	Gln	Phe	Thr	Leu	Asn	Phe	Val	Glu	Phe	Asn	Leu	Glu	Lys	
				185					190					195	
His	Arg	Ser	Ser	Ser	Thr	Thr	Glu	Ile	Glu	Ile	Ile	Ala	Pro	His	
				200					205					210	

Lys	Val	Val	Glu	Arg	Thr	Gln	Asn	Val	Thr	Glu	Lys	Val	Thr	Gln
				215					220					225
Val	Leu	Ser	Leu	Gly	Ala	Asp	Val	Leu	Pro	Glu	Tyr	Lys	Leu	Gln
				230					235					240
Ala	Pro	Arg	Ile	His	Arg	Trp	Thr	Ile	Leu	His	Tyr	Ser	Pro	Phe
				245					250					255
Lys	Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu	Leu	Val	Ile	Tyr	Thr
				260					265					270
Ala	Val	Phe	Thr	Pro	Tyr	Ser	Ala	Ala	Phe	Leu	Leu	Ser	Asp	Gln
				275					280					285
Asp	Glu	Ser	Arg	Arg	Gly	Ala	Cys	Ser	Tyr	Thr	Cys	Ser	Pro	Leu
				290					295					300
Thr	Val	Val	Asp	Leu	Ile	Val	Asp	Ile	Met	Phe	Val	Val	Asp	Ile
				305					310					315
Val	Ile	Asn	Phe	Arg	Thr	Thr	Tyr	Val	Asn	Thr	Asn	Asp	Glu	Val
				320					325					330
Val	Ser	His	Pro	Arg	Arg	Ile	Ala	Val	His	Tyr	Phe	Lys	Gly	Trp
				335					340					345
Phe	Leu	Ile	Asp	Met	Val	Ala	Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile
				350					355					360
Phe	Arg	Thr	Gly	Ser	Asp	Glu	Thr	Thr	Thr	Leu	Ile	Gly	Leu	Leu
				365					370					375
Lys	Thr	Ala	Arg	Leu	Leu	Arg	Leu	Val	Arg	Val	Ala	Arg	Lys	Leu
				380					385					390
Asp	Arg	Tyr	Ser	Glu	Tyr	Gly	Ala	Ala	Val	Leu	Phe	Leu	Leu	Met
				395					400					405
Cys	Thr	Phe	Pro	Leu	Ile	Ala	His	Trp	Leu	Ala	Cys	Ile	Trp	Tyr
				410					415					420
Ala	Ile	Gly	Asn	Val	Glu	Arg	Pro	Tyr	Leu	Glu	His	Lys	Ile	Gly
				425					430					435
Trp	Leu	Asp	Ser	Leu	Gly	Val	Gln	Leu	Gly	Lys	Arg	Tyr	Asn	Gly
				440					445					450
Ser	Asp	Pro	Ala	Ser	Gly	Pro	Ser	Val	Gln	Asp	Lys	Tyr	Val	Thr
				455					460					465
Ala	Leu	Tyr	Phe	Thr	Phe	Ser	Ser	Leu	Thr	Ser	Val	Gly	Phe	Gly
				470					475					480
Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu	Lys	Val	Phe	Ser	Ile	Cys
				485					490					495
Val	Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	Phe	Gly	Asn
				500					505					510
Val	Ser	Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	Arg	Tyr
				515					520					525
His	Thr	Gln	Met	Leu	Arg	Val	Lys	Glu	Phe	Ile	Arg	Phe	His	Gln
				530					535					540
Ile	Pro	Asn	Pro	Leu	Arg	Gln	Arg	Leu	Glu	Glu	Tyr	Phe	Gln	His
				545					550					555
Ala	Trp	Ser	Tyr	Thr	Asn	Gly	Ile	Asp	Met	Asn	Ala	Val	Leu	Lys
				560					565					570
Gly	Phe	Pro	Glu	Cys	Leu	Gln	Ala	Asp	Ile	Cys	Leu	His	Leu	His
				575					580					585
Arg	Ala	Leu	Leu	Gln	His	Cys	Pro	Ala	Phe	Ser	Gly	Ala	Gly	Lys
				590					595					600
Gly	Cys	Leu	Arg	Ala	Leu	Ala	Val	Lys	Phe	Lys	Thr	Thr	His	Ala
				605					610					615
Pro	Pro	Gly	Asp	Thr	Leu	Val	His	Leu	Gly	Asp	Val	Leu	Ser	Thr
				620					625					630
Leu	Tyr	Phe	Ile	Ser	Arg	Gly	Ser	Ile	Glu	Ile	Leu	Arg	Asp	Asp
				635					640					645
Val	Val	Val	Ala	Ile	Leu	Gly	Lys	Asn	Asp	Ile	Phe	Gly	Glu	Pro
				650					655					660
Val	Ser	Leu	His	Ala	Gln	Pro	Gly	Lys	Ser	Ser	Ala	Asp	Val	Arg
				665					670					675
Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	Ile	Gln	Arg	Ala	Asp	Leu
				680					685					690
Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Ala	Phe	Ala	Glu	Ser	Phe	Trp
				695					700					705
Ser	Lys	Leu	Glu	Val	Thr	Phe	Asn	Leu	Arg	Asp	Val	Thr	Gly	Gly

Leu His Ser Ser	710	715	720
Pro Arg Gln Ala Pro Gly Ser Gln Asp His Gln			
Gly Phe Phe Leu	725	730	735
Ser Asp Asn Gln Ser Asp Ala Ala Pro Pro Leu			
Ser Ile Ser Asp	740	745	750
Ala Phe Trp Leu Trp Pro Glu Leu Leu Gln Glu			
Met Pro Pro Lys	755	760	765
His Ser Pro Gln Ser Pro Gln Glu Asp Pro Asp			
Cys Trp Pro Leu	770	775	780
Lys Leu Gly Ser Arg Leu Glu Gln Leu Gln Ala			
Gln Met Asn Arg	785	790	795
Leu Glu Ser Arg Val Ser Ser Asp Leu Ser Arg			
Ile Leu Gln Leu	800	805	810
Leu Gln Lys Pro Met Pro Gln Gly His Ala Ser			
Tyr Ile Leu Glu	815	820	825
Ala Pro Ala Ser Asn Asp Leu Ala Leu Val Pro			
Ile Ala Ser Glu	830	835	840
Thr Thr Ser Pro Gly Pro Arg Leu Pro Gln Gly			
Phe Leu Pro Pro	845	850	855
Ala Gln Thr Pro Ser Tyr Gly Asp Leu Asp Asp			
Cys Ser Pro Lys	860	865	870
His Arg Asn Ser Ser Pro Arg Met Pro His Leu			
Ala Val Ala Met	875	880	885
Asp Lys Thr Leu Ala Pro Ser Ser Glu Gln Glu			
Gln Pro Glu Gly	890	895	900
Leu Trp Pro Pro Leu Ala Ser Pro Leu His Pro			
Leu Glu Val Gln	905	910	915
Gly Leu Ile Cys Gly Pro Cys Phe Ser Ser Leu			
Pro Glu His Leu	920	925	930
Gly Ser Val Pro Lys Gln Leu Asp Phe Gln Arg			
His Gly Ser Asp	935	940	945
Pro Gly Phe Ala Gly Ser Trp Gly His			
	950	955	

<210> 10

<211> 724

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7472728CD1

<400> 10

Met Gly His Gln Gly	Pro Phe Glu Glu Gly	Asn Gly Gly Leu Arg
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Val Ile Ala Thr Trp	Arg Arg Lys Glu Ala	Trp Arg Arg Asp Cys
20	25	30
Leu Leu Gly Ala Leu	Pro Ser Val Ser Cys	Gly Gly Trp Gly His
35	40	45
Arg Gly Arg Gln Thr	Tyr Gly Arg Ala Cys	Gly Val Lys Glu Lys
50	55	60
Pro Phe Ser Leu Leu	Gly Pro Gln Ile Thr	Val Tyr Ala Val Trp
65	70	75
Pro Gln Ser Glu Gly	Pro Gln Glu Gly Arg	Leu Arg Val Asn Ser
80	85	90
Ala Cys Leu Pro Pro	Glu Arg Gly Leu Thr	Asn Ala Cys Thr Asn
95	100	105
His Glu Glu Leu Ser	Leu Asp Cys Leu Leu	Phe Glu Asn Val Asn
110	115	120
Thr Leu Thr Leu Asp	Phe Cys Leu Trp Glu	Lys Thr Thr Ile Val
125	130	135
Pro Gly Val Leu Pro	Tyr Ala Gly Leu Thr	Leu Gln Ser Lys Phe
140	145	150
Leu Leu Gly Arg Ala	Leu Leu Ala Gly Val	His Val Ile Thr Leu
155	160	165
Thr Pro Glu Arg Val	Thr His His Val His	Gly Trp Tyr Met Glu

	170		175		180
Asp Gly Phe Lys	Gly Asp Arg Thr Glu	Gly Cys Arg Ser Asp	Ser		
	185		190		195
Val Ala Val Pro	Ala Ala Ala Pro Val	Cys Gln Pro Lys Ser	Ala		
	200		205		210
Thr Asn Gly Gln	Pro Pro Ala Pro Ala	Pro Thr Pro Thr Pro	Arg		
	215		220		225
Leu Ser Ile Ser	Ser Arg Ala Thr Val	Val Ala Arg Met Glu	Gly		
	230		235		240
Thr Ser Gln Gly	Gly Leu Gln Thr Val	Met Lys Trp Lys Thr	Val		
	245		250		255
Val Ala Ile Phe	Val Val Val Val Val	Tyr Leu Val Thr Gly	Gly		
	260		265		270
Leu Val Phe Arg	Ala Leu Glu Gln Pro	Phe Glu Ser Ser Gln	Lys		
	275		280		285
Asn Thr Ile Ala	Leu Glu Lys Ala Glu	Phe Leu Arg Asp His	Val		
	290		295		300
Cys Val Ser Pro	Gln Glu Leu Glu Thr	Leu Ile Gln His Ala	Leu		
	305		310		315
Asp Ala Asp Asn	Ala Gly Val Ser Pro	Ile Gly Asn Ser Ser	Asn		
	320		325		330
Asn Ser Ser His	Trp Asp Leu Gly Ser	Ala Phe Phe Phe Ala	Gly		
	335		340		345
Thr Val Ile Thr	Thr Met Tyr Gly Asn	Ile Ala Pro Ser Thr	Glu		
	350		355		360
Gly Gly Lys Ile	Phe Cys Ile Leu Tyr	Ala Ile Phe Gly Ile	Pro		
	365		370		375
Leu Phe Gly Phe	Leu Leu Ala Gly Ile	Gly Asp Gln Leu Gly	Thr		
	380		385		390
Ile Phe Gly Lys	Ser Ile Ala Arg Val	Glu Lys Val Phe Arg	Lys		
	395		400		405
Lys Gln Val Ser	Gln Thr Lys Ile Arg	Val Ile Ser Thr Ile	Leu		
	410		415		420
Phe Ile Leu Ala	Gly Cys Ile Val Phe	Val Thr Ile Pro Ala	Val		
	425		430		435
Ile Phe Lys Tyr	Ile Glu Gly Trp Thr	Ala Leu Glu Ser Ile	Tyr		
	440		445		450
Phe Val Val Val	Thr Leu Thr Thr Val	Gly Phe Gly Asp Phe	Val		
	455		460		465
Ala Val Val Val	Phe Arg Gly Asn Ala	Gly Ile Asn Tyr Arg	Glu		
	470		475		480
Trp Tyr Lys Pro	Leu Val Trp Phe Trp	Ile Leu Val Gly Leu	Ala		
	485		490		495
Tyr Phe Ala Ala	Val Leu Ser Met Ile	Gly Asp Trp Leu Arg	Val		
	500		505		510
Leu Ser Lys Lys	Thr Lys Glu Glu Val	Gly Glu Ile Lys Ala	His		
	515		520		525
Ala Ala Glu Trp	Lys Ala Asn Val Thr	Ala Glu Phe Arg Glu	Thr		
	530		535		540
Arg Arg Arg Leu	Ser Val Glu Ile His	Asp Lys Leu Gln Arg	Ala		
	545		550		555
Ala Thr Ile Arg	Ser Met Glu Arg Arg	Arg Leu Gly Leu Asp	Gln		
	560		565		570
Arg Ala His Ser	Leu Asp Met Leu Ser	Pro Glu Lys Arg Ser	Val		
	575		580		585
Phe Ala Ala Leu	Asp Thr Gly Arg Phe	Lys Ala Ser Ser Gln	Glu		
	590		595		600
Ser Ile Asn Asn	Arg Pro Asn Asn Leu	Arg Leu Lys Gly Pro	Glu		
	605		610		615
Gln Leu Asn Lys	His Gly Gln Gly Ala	Ser Glu Asp Asn Ile	Ile		
	620		625		630
Asn Lys Phe Gly	Ser Thr Ser Arg Leu	Thr Lys Arg Lys Asn	Lys		
	635		640		645
Asp Leu Lys Lys	Thr Leu Pro Glu Asp	Val Gln Lys Ile Tyr	Lys		
	650		655		660
Thr Phe Arg Asn	Tyr Ser Leu Asp Glu	Glu Lys Lys Glu Glu	Glu		
	665		670		675

Thr	Glu	Lys	Met	Cys	Asn	Ser	Asp	Asn	Ser	Ser	Thr	Ala	Met	Leu
				680					685					690
Thr	Asp	Cys	Ile	Gln	His	Ala	Glu	Leu	Glu	Asn	Gly	Met	Ile	
				695				700						705
Pro	Thr	Asp	Thr	Lys	Asp	Arg	Glu	Pro	Glu	Asn	Asn	Ser	Leu	Leu
				710					715					720
Glu	Asp	Arg	Asn											

<210> 11

<211> 470

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474322CD1

<220>

<221> unsure

<222> 253

<223> unknown or other

<400> 11

Met	Tyr	Asn	Glu	Ile	Leu	Met	Leu	Gly	Ala	Lys	Leu	His	Pro	Thr
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Leu	Lys	Leu	Glu	Glu	Leu	Thr	Asn	Lys	Lys	Gly	Met	Thr	Pro	Leu
				20					25					30
Ala	Leu	Ala	Ala	Gly	Thr	Gly	Lys	Ile	Gly	Asn	Arg	His	Asp	Met
				35					40					45
Leu	Leu	Val	Glu	Pro	Leu	Asn	Arg	Leu	Leu	Gln	Asp	Lys	Trp	Asp
				50					55					60
Arg	Phe	Val	Lys	Arg	Ile	Phe	Tyr	Phe	Asn	Phe	Leu	Val	Tyr	Cys
				65					70					75
Leu	Tyr	Met	Ile	Ile	Phe	Thr	Met	Ala	Ala	Tyr	Tyr	Arg	Pro	Val
				80					85					90
Asp	Gly	Leu	Pro	Pro	Phe	Lys	Met	Glu	Lys	Thr	Gly	Asp	Tyr	Phe
				95					100					105
Arg	Val	Thr	Gly	Glu	Ile	Leu	Ser	Val	Leu	Gly	Gly	Val	Tyr	Phe
				110					115					120
Phe	Phe	Arg	Gly	Ile	Gln	Tyr	Phe	Leu	Gln	Arg	Arg	Pro	Ser	Met
				125					130					135
Lys	Thr	Leu	Phe	Val	Asp	Ser	Tyr	Ser	Glu	Met	Leu	Leu	Phe	Leu
				140					145					150
Gln	Ser	Leu	Phe	Met	Leu	Ala	Thr	Val	Val	Leu	Tyr	Phe	Ser	His
				155					160					165
Leu	Lys	Glu	Tyr	Val	Ala	Ser	Met	Val	Phe	Ser	Leu	Ala	Leu	Gly
				170					175					180
Trp	Thr	Asn	Met	Leu	Tyr	Tyr	Thr	Arg	Gly	Phe	Gln	Gln	Met	Gly
				185					190					195
Ile	Tyr	Ala	Val	Met	Ile	Glu	Lys	Met	Ile	Leu	Arg	Asp	Leu	Cys
				200					205					210
Arg	Phe	Met	Phe	Val	Tyr	Ile	Val	Phe	Leu	Phe	Gly	Phe	Ser	Thr
				215					220					225
Ala	Val	Val	Thr	Leu	Ile	Glu	Asp	Gly	Lys	Asn	Asp	Ser	Leu	Pro
				230					235					240
Ser	Glu	Ser	Thr	Ser	His	Arg	Trp	Arg	Gly	Pro	Ala	Xaa	Arg	Pro
				245					250					255
Asn	Ser	Ser	Tyr	Asn	Ser	Leu	Tyr	Ser	Thr	Cys	Leu	Glu	Leu	Phe
				260					265					270
Lys	Phe	Thr	Ile	Gly	Met	Gly	Asp	Leu	Glu	Phe	Thr	Glu	Asn	Tyr
				275					280					285
Asp	Phe	Lys	Ala	Val	Phe	Ile	Ile	Leu	Leu	Leu	Ala	Tyr	Val	Ile
				290					295					300
Leu	Thr	Tyr	Ile	Val	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu	Met
				305					310					315
Gly	Glu	Thr	Val	Glu	Asn	Val	Ser	Lys	Glu	Ser	Glu	Arg	Ile	Trp

320	325	330
Arg Leu Gln Arg	Ala Ile Thr Ile Leu Asp Thr Glu Lys Ser	Phe
335	340	345
Leu Lys Cys Met	Arg Lys Ala Phe Arg Ser Gly Lys Leu Leu	Gln
350	355	360
Val Gly Tyr Thr	Pro Asp Gly Lys Asp Asp Tyr Arg Trp Cys	Phe
365	370	375
Val Asp Glu Val	Asn Trp Thr Thr Trp Asn Thr Asn Val Gly	Ile
380	385	390
Ile Asn Glu Asp	Pro Gly Asn Cys Glu Gly Val Lys Arg Thr	Leu
395	400	405
Ser Phe Ser Leu	Arg Ser Ser Arg Val Ser Gly Arg His Trp	Lys
410	415	420
Asn Phe Ala Leu	Val Pro Leu Leu Arg Glu Ala Ser Ala Arg	Asp
425	430	435
Arg Gln Ser Ala	Gln Pro Glu Glu Val Tyr Leu Arg Gln Phe	Ser
440	445	450
Gly Ser Leu Lys	Pro Glu Asp Ala Glu Val Phe Lys Ser Pro	Ala
455	460	465
Ala Ser Gly Glu	Lys	
470		

<210> 12

<211> 618

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5455621CD1

<400> 12

Met Glu Val Lys	Asn Phe Ala Val Trp Asp Tyr Val Val Phe	Ala
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Ala Leu Phe Phe	Ile Ser Ser Gly Ile Gly Val Phe Phe	Ala
20	25	30
Lys Glu Arg Lys	Lys Ala Thr Ser Arg Glu Phe Leu Val Gly	Gly
35	40	45
Arg Gln Met Ser	Phe Gly Pro Val Gly Leu Ser Leu Thr Ala	Ser
50	55	60
Phe Met Ser Ala	Val Thr Val Leu Gly Thr Pro Ser Glu Val	Tyr
65	70	75
Arg Phe Gly Ala	Ser Phe Leu Val Phe Phe Ile Ala Tyr Leu	Phe
80	85	90
Val Ile Leu Leu	Thr Ser Glu Leu Phe Leu Pro Val Phe Tyr	Arg
95	100	105
Ser Gly Ile Thr	Ser Thr Tyr Glu Tyr Leu Gln Leu Arg Phe	Asn
110	115	120
Lys Pro Val Arg	Tyr Ala Ala Thr Val Ile Tyr Ile Val Gln	Thr
125	130	135
Ile Leu Tyr Thr	Gly Val Val Val Tyr Ala Pro Ala Leu Ala	Leu
140	145	150
Asn Gln Val Thr	Gly Phe Asp Leu Trp Gly Ser Val Phe Ala	Thr
155	160	165
Gly Ile Val Cys	Thr Phe Tyr Cys Thr Leu Gly Gly Leu Lys	Ala
170	175	180
Val Val Trp Thr	Asp Ala Phe Gln Met Val Val Met Ile Val	Gly
185	190	195
Phe Leu Thr Val	Leu Ile Gln Gly Ser Thr His Ala Gly Gly	Phe
200	205	210
His Asn Val Leu	Glu Gln Ser Thr Asn Gly Ser Arg Leu His	Ile
215	220	225
Phe Asp Phe Asp	Val Asp Pro Leu Arg Arg His Thr Phe Trp	Thr
230	235	240
Ile Thr Val Gly	Gly Thr Phe Thr Trp Leu Gly Ile Tyr Gly	Val
245	250	255
Asn Gln Ser Thr	Ile Gln Arg Cys Ile Ser Cys Lys Thr Glu	Lys

His Ala Lys Leu	260	Ala Leu Tyr Phe Asn	265	Leu Leu Gly Leu Trp	270
Ile Leu Val Cys	275	Ala Val Phe Ser Gly	280	Ile Met Tyr Ser	285
Phe Lys Asp Cys	290	Asp Pro Trp Thr Ser	295	Ile Ile Ser Ala	300
Asp Gln Leu Met	305	Pro Tyr Phe Val Met	310	Ile Phe Ala Thr	315
Pro Gly Leu Pro	320	Gly Leu Phe Val Ala	325	Cys Ala Phe Ser	330
Leu Ser Thr Val	335	Ala Ser Ser Ile Asn	340	Ala Leu Ala Thr	345
Phe Glu Asp Phe	350	Val Lys Ser Cys Phe	355	Pro His Leu Ser	360
Leu Ser Thr Trp	365	Ile Ser Lys Gly Leu	370	Cys Leu Leu Phe	375
Met Cys Thr Ser	380	Met Ala Val Ala Ala	385	Val Met Gly Gly	390
Val Gln Ala Ser	395	Leu Ser Ile His Gly	400	Met Cys Gly Gly	405
Leu Gly Leu Phe	410	Ser Leu Gly Ile Val	415	Pro Phe Val Asn	420
Lys Gly Ala Leu	425	Gly Gly Leu Leu Thr	430	Gly Ile Thr Leu	435
Trp Val Ala Ile	440	Gly Ala Phe Ile Tyr	445	Pro Ala Pro Ala	450
Thr Trp Pro Leu	455	Pro Leu Ser Thr Asp	460	Gln Cys Ile Lys	465
Val Thr Ala Thr	470	Gly Pro Pro Val Leu	475	Ser Ser Arg Pro	480
Ala Asp Thr Trp	485	Tyr Ser Ile Ser Tyr	490	Leu Tyr Tyr Ser	495
Gly Cys Leu Gly	500	Cys Ile Val Ala Gly	505	Val Ile Ile Ser	510
Thr Gly Arg Gln	515	Arg Gly Glu Asp Ile	520	Gln Pro Leu Leu	525
Pro Val Cys Asn	530	Leu Phe Cys Phe Trp	535	Ser Lys Lys Tyr	540
Leu Cys Trp Cys	545	Gly Val Gln His Asp	550	Ser Gly Thr Glu	555
Asn Leu Glu Asn	560	Gly Ser Ala Arg Lys	565	Gln Gly Ala Glu	570
Leu Gln Asn Gly	575	Leu Arg Arg Glu Ser	580	Val His Val Pro	585
Tyr Asp Pro Lys	590	Asp Lys Ser Tyr Asn	595	Asn Met Ala Phe	600
Thr His Phe	605		610	Glu Thr	615

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 <223> Incyte ID No: 7477248CD1

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 20 25 30
 Leu Ile Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg
 35 40 45
 Phe Arg Phe Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu

Ile Met Gly Leu	50	Leu Arg Tyr Ala	55	Thr Ala Pro Thr Asp	60
	65		70		75
Glu Ser Gly Thr	80	Val Tyr Asp Cys Val	85	Lys Leu Thr Phe Ser	90
Ser Thr Leu Leu	95	Val Asn Ile Thr Asp	100	Gln Val Tyr Glu Tyr	105
Tyr Lys Arg Glu	110	Ile Ser Gln His Asn	115	Ile Asn Pro His Gln	120
Asn Ala Ile Leu	125	Glu Lys Met Thr Phe	130	Asp Pro Glu Ile Phe	135
Asn Val Leu Leu	140	Pro Pro Ile Ile Phe	145	His Ala Gly Tyr Ser	150
Lys Lys Arg His	155	Phe Phe Gln Asn Leu	160	Gly Ser Ile Leu Thr	165
Ala Phe Leu Gly	170	Thr Ala Ile Ser Cys	175	Ile Val Ile Gly Leu	180
Met Tyr Gly Phe	185	Val Lys Ala Met Ile	190	His Ala Gly Gln Leu	195
Asn Gly Asp Phe	200	His Phe Thr Asp Cys	205	Leu Phe Phe Gly Ser	210
Met Ser Ala Thr	215	Asp Pro Val Thr Val	220	Leu Ala Ile Phe His	225
Leu His Val Asp	230	Pro Asp Leu Tyr Thr	235	Leu Leu Phe Gly Glu	240
Val Leu Asn Asp	245	Ala Val Ala Ile Val	250	Leu Thr Tyr Ser Ile	255
Ile Tyr Ser Pro	260	Lys Glu Asn Pro Asn	265	Ala Phe Asp Ala Ala	270
Phe Phe Gln Ser	275	Val Gly Asn Phe Leu	280	Gly Ile Phe Ala Gly	285
Phe Ala Met Gly	290	Ser Ala Tyr Ala Ile	295	Ile Thr Ala Leu Leu	300
Lys Phe Thr Lys	305	Leu Cys Glu Phe Pro	310	Met Leu Glu Thr Gly	315
Phe Phe Leu Leu	320	Ser Trp Ser Ala Phe	325	Leu Ser Ala Glu Ala	330
Gly Leu Thr Gly	335	Ile Val Ala Val Leu	340	Phe Cys Gly Val Thr	345
Ala His Tyr Thr	350	Tyr Asn Asn Leu Ser	355	Ser Asp Ser Lys Ile	360
Thr Lys Gln Leu	365	Phe Glu Phe Met Asn	370	Phe Leu Ala Glu Asn	375
Ile Phe Cys Tyr	380	Met Gly Leu Ala Leu	385	Phe Thr Phe Gln Asn	390
Ile Phe Asn Ala	395	Leu Phe Ile Leu Gly	400	Ala Phe Leu Ala Ile	405
Val Ala Arg Ala	410	Cys Asn Ile Tyr Pro	415	Leu Ser Phe Leu Leu	420
Leu Gly Arg Lys	425	Gln Lys Ile Pro Trp	430	Asn Phe Gln His Met	435
Met Phe Ser Gly	440	Leu Arg Gly Ala Ile	445	Ala Phe Ala Leu Ala	450
Arg Asn Thr Glu	455	Ser Gln Pro Lys Gln	460	Met Met Phe Thr Thr	465
Leu Leu Leu Val	470	Phe Phe Thr Val Trp	475	Val Phe Gly Gly Gly	480
Thr Pro Met Leu	485	Thr Trp Leu Gln Ile	490	Arg Val Gly Val Asp	495
Asp Glu Asn Leu	500	Lys Glu Asp Pro Ser	505	Ser Gln His Gln Glu	510
Asn Asn Leu Asp	515	Lys Asn Met Thr Lys	520	Ala Glu Ser Ala Arg	525
Phe Arg Met Trp	530	Tyr Ser Phe Asp His	535	Lys Tyr Leu Lys Pro	540
Leu Thr His Ser	545	Gly Pro Pro Leu Thr	550	Thr Thr Leu Pro Glu	555

Cys	Gly	Pro	Ile	Ser	Arg	Leu	Leu	Thr	Ser	Pro	Gln	Ala	Tyr	Gly
				560					565					570
Glu	Gln	Leu	Lys	Glu	Asp	Asp	Val	Glu	Cys	Ile	Val	Asn	Gln	Asp
				575					580					585
Glu	Leu	Ala	Ile	Asn	Tyr	Gln	Glu	Gln	Ala	Ser	Ser	Pro	Cys	Ser
				590					595					600
Pro	Pro	Ala	Arg	Leu	Gly	Leu	Asp	Gln	Lys	Ala	Ser	Pro	Gln	Thr
				605					610					615
Pro	Gly	Lys	Glu	Asn	Ile	Tyr	Glu	Gly	Asp	Leu	Gly	Pro	Gly	Arg
				620					625					630
Leu														

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<220>
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Glu	Met	Glu	Ile	Tyr	Gly	Tyr	Asn	Leu	Ser	Arg	Trp	Lys	Leu	Ala
				20					25					30
Ile	Val	Ser	Leu	Gly	Val	Ile	Cys	Ser	Gly	Gly	Val	Ser	Pro	Pro
				35					40					45
Pro	Leu	Tyr	Trp	Met	Pro	Glu	Trp	Arg	Val	Lys	Ala	Thr	Cys	Val
				50					55					60
Arg	Ala	Ala	Ile	Lys	Asp	Cys	Glu	Val	Val	Leu	Leu	Arg	Thr	Thr
				65					70					75
Asp	Glu	Phe	Lys	Met	Trp	Phe	Cys	Ala	Lys	Ile	Arg	Val	Leu	Ser
				80					85					90
Leu	Glu	Thr	Tyr	Pro	Val	Ser	Ser	Pro	Lys	Ser	Met	Ser	Asn	Lys
				95					100					105
Leu	Ser	Asn	Gly	His	Ala	Val	Cys	Leu	Ile	Glu	Asn	Pro	Thr	Glu
				110					115					120
Glu	Asn	Arg	His	Arg	Ile	Ser	Lys	Tyr	Ser	Gln	Thr	Glu	Ser	Gln
				125					130					135
Gln	Ile	Arg	Tyr	Phe	Thr	His	His	Ser	Val	Lys	Tyr	Phe	Trp	Asn
				140					145					150
Asp	Thr	Ile	His	Asn	Phe	Asp	Phe	Leu	Lys	Gly	Leu	Asp	Glu	Gly
				155					160					165
Val	Ser	Cys	Thr	Ser	Ile	Tyr	Glu	Lys	His	Ser	Ala	Gly	Leu	Thr
				170					175					180
Lys	Gly	Met	His	Ala	Tyr	Arg	Lys	Leu	Leu	Tyr	Gly	Val	Asn	Glu
				185					190					195
Ile	Ala	Val	Lys	Val	Pro	Ser	Val	Phe	Lys	Leu	Leu	Ile	Lys	Glu
				200					205					210
Val	Leu	Asn	Pro	Phe	Tyr	Ile	Phe	Gln	Leu	Phe	Ser	Val	Ile	Leu
				215					220					225
Trp	Ser	Thr	Asp	Glu	Tyr	Tyr	Tyr	Tyr	Ala	Leu	Ala	Ile	Val	Val
				230					235					240
Met	Ser	Ile	Val	Ser	Ile	Val	Ser	Ser	Leu	Tyr	Ser	Ile	Arg	Lys
				245					250					255
Gln	Tyr	Val	Met	Leu	His	Asp	Met	Val	Ala	Thr	His	Ser	Thr	Val
				260					265					270
Arg	Val	Ser	Val	Cys	Arg	Val	Asn	Glu	Glu	Ile	Glu	Glu	Ile	Phe
				275					280					285
Ser	Thr	Asp	Leu	Val	Pro	Gly	Asp	Val	Met	Val	Ile	Pro	Leu	Asn
				290					295					300
Gly	Thr	Ile	Met	Pro	Cys	Asp	Ala	Val	Leu	Ile	Asn	Gly	Thr	Cys
				305					310					315
Ile	Val	Asn	Glu	Ser	Met	Leu	Thr	Gly	Glu	Ser	Val	Pro	Val	Thr
				320					325					330

Lys	Thr	Asn	Leu	Pro	Asn	Pro	Ser	Val	Asp	Val	Lys	Gly	Ile	Gly
				335					340					345
Asp	Glu	Leu	Tyr	Asn	Pro	Glu	Thr	His	Lys	Arg	His	Thr	Leu	Phe
				350					355					360
Cys	Gly	Thr	Thr	Val	Ile	Gln	Thr	Arg	Phe	Tyr	Thr	Gly	Glu	Leu
				365					370					375
Val	Lys	Ala	Ile	Val	Val	Arg	Thr	Gly	Phe	Ser	Thr	Ser	Lys	Gly
				380					385					390
Gln	Leu	Val	Arg	Ser	Ile	Leu	Tyr	Pro	Lys	Pro	Thr	Asp	Phe	Lys
				395					400					405
Leu	Tyr	Arg	Asp	Ala	Tyr	Leu	Phe	Leu	Leu	Cys	Leu	Val	Ala	Val
				410					415					420
Ala	Gly	Ile	Gly	Phe	Ile	Tyr	Thr	Ile	Ile	Asn	Ser	Ile	Leu	Asn
				425					430					435
Glu	Val	Gln	Val	Gly	Val	Ile	Ile	Ile	Glu	Ser	Leu	Asp	Ile	Ile
				440					445					450
Thr	Ile	Thr	Val	Pro	Pro	Ala	Leu	Pro	Ala	Ala	Met	Thr	Ala	Gly
				455					460					465
Ile	Val	Tyr	Ala	Gln	Arg	Arg	Leu	Lys	Lys	Ile	Gly	Ile	Phe	Cys
				470					475					480
Ile	Ser	Pro	Gln	Arg	Ile	Asn	Ile	Cys	Gly	Gln	Leu	Asn	Leu	Val
				485					490					495
Cys	Phe	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Glu	Asp	Gly	Leu	Asp	Leu
				500					505					510
Trp	Gly	Ile	Gln	Arg	Val	Glu	Asn	Ala	Arg	Phe	Leu	Ser	Pro	Glu
				515					520					525
Glu	Asn	Val	Cys	Asn	Glu	Met	Leu	Val	Lys	Ser	Gln	Phe	Val	Ala
				530					535					540
Cys	Met	Ala	Thr	Cys	His	Ser	Leu	Thr	Lys	Ile	Glu	Gly	Val	Leu
				545					550					555
Ser	Gly	Asp	Pro	Leu	Asp	Leu	Lys	Met	Phe	Glu	Ala	Ile	Gly	Trp
				560					565					570
Ile	Leu	Glu	Glu	Ala	Thr	Glu	Glu	Glu	Thr	Ala	Leu	His	Asn	Arg
				575					580					585
Ile	Met	Pro	Thr	Val	Val	Arg	Pro	Pro	Lys	Gln	Leu	Leu	Pro	Glu
				590					595					600
Ser	Thr	Pro	Ala	Gly	Asn	Gln	Glu	Met	Glu	Leu	Phe	Glu	Leu	Pro
				605					610					615
Ala	Thr	Tyr	Glu	Ile	Gly	Ile	Val	Arg	Gln	Phe	Pro	Phe	Ser	Ser
				620					625					630
Ala	Leu	Gln	Arg	Met	Ser	Val	Val	Ala	Arg	Val	Leu	Gly	Asp	Arg
				635					640					645
Lys	Met	Asp	Ala	Tyr	Met	Lys	Gly	Ala	Pro	Glu	Ala	Ile	Ala	Gly
				650					655					660
Leu	Cys	Lys	Pro	Glu	Thr	Val	Pro	Val	Asp	Phe	Gln	Asn	Val	Leu
				665					670					675
Glu	Asp	Phe	Thr	Lys	Gln	Gly	Phe	Arg	Val	Ile	Ala	Leu	Ala	His
				680					685					690
Arg	Lys	Leu	Glu	Ser	Lys	Leu	Thr	Trp	His	Lys	Val	Gln	Asn	Ile
				695					700					705
Ser	Arg	Asp	Ala	Ile	Glu	Asn	Asn	Met	Asp	Phe	Met	Gly	Leu	Ile
				710					715					720
Ile	Met	Gln	Asn	Lys	Leu	Lys	Gln	Lys	Thr	Pro	Ala	Val	Leu	Glu
				725					730					735
Asp	Leu	His	Lys	Ala	Asn	Ile	Arg	Thr	Val	Met	Val	Thr	Gly	Asp
				740					745					750
Ser	Met	Leu	Thr	Ala	Val	Ser	Val	Ala	Arg	Asp	Cys	Gly	Met	Ile
				755					760					765
Leu	Pro	Gln	Asp	Lys	Val	Ile	Ile	Ala	Glu	Ala	Leu	Pro	Pro	Lys
				770					775					780
Asp	Gly	Lys	Val	Ala	Lys	Ile	Asn	Trp	His	Tyr	Ala	Asp	Ser	Leu
				785					790					795
Thr	Gln	Cys	Ser	His	Pro	Ser	Ala	Ile	Asp	Pro	Glu	Ala	Ile	Pro
				800					805					810
Val	Lys	Leu	Val	His	Asp	Ser	Leu	Glu	Asp	Leu	Gln	Met	Thr	Arg
				815					820					825
Tyr	His	Phe	Ala	Met	Asn	Gly	Lys	Ser	Phe	Ser	Val	Ile	Leu	Glu

His Phe Gln Asp	830	Val Pro Lys Leu	835	Leu His Gly Thr	840
Phe Ala Arg Met	845	Pro Asp Gln Lys	850	Gln Leu Ile Glu	855
Leu Gln Asn Val	860	Tyr Phe Val Gly	865	Met Cys Gly Asp Gly	870
Asn Asp Cys Gly	875	Leu Lys Arg Ala	880	His Gly Gly Ile Ser	885
Ser Glu Leu Glu	890	Ser Val Ala Ser	895	Pro Phe Thr Ser Lys	900
Pro Ser Ile Ser	905	Cys Val Pro Asn Leu	910	Arg Glu Gly Arg	915
Ala Leu Ile Thr	920	Phe Cys Val Phe	925	Lys Phe Met Ala Leu	930
Ser Ile Ile Gln	935	Tyr Phe Ser Val Thr	940	Leu Leu Tyr Ser Ile	945
Ser Asn Leu Gly	950	Asp Phe Gln Phe Leu	955	Phe Ile Asp Leu Ala	960
Ile Leu Val Val	965	Val Phe Thr Met Ser	970	Leu Asn Pro Ala Trp	975
Glu Leu Val Ala	980	Gln Arg Pro Pro Ser	985	Gly Leu Ile Ser Gly	990
Leu Leu Phe Ser	995	Val Leu Ser Gln Ile	1000	Ile Ile Cys Ile Gly	1005
Gln Ser Leu Gly	1010	Phe Phe Trp Val Lys	1015	Gln Gln Pro Trp Tyr	1020
Val Trp His Pro	1025	Lys Ser Asp Ala Cys	1030	Asn Thr Thr Gly Ser	1035
Phe Trp Asn Ser	1040	Thr His Val Asp Asn	1045	Glu Thr Glu Leu Asp	1050
His Asn Ile Gln	1055	Ser Tyr Glu Asn Thr	1060	Thr Val Phe Phe Ile	1065
Ser Phe Gln Tyr	1070	Leu Ile Val Ala Ile	1075	Phe Ser Lys Gly Lys	1080
Pro Phe Arg Gln	1085	Pro Cys Tyr Lys Asn	1090	Tyr Phe Phe Val Phe	1095
Val Ile Phe Leu	1100	Tyr Ile Phe Ile Leu	1105	Phe Ile Met Leu Tyr	1110
Val Ala Ser Val	1115	Asp Gln Val Leu Gln	1120	Ile Val Cys Val Pro	1125
Gln Trp Arg Val	1130	Thr Met Leu Ile Ile	1135	Val Leu Val Asn Ala	1140
Val Ser Ile Thr	1145	Val Glu Asn Phe Phe	1150	Leu Asp Met Val Leu	1155
Lys Val Val Phe	1160	Asn Arg Asp Lys Gln	1165	Gly Glu Tyr Arg Phe	1170
Thr Thr Gln Pro	1175	Pro Gln Glu Ser Val	1180	Asp Arg Trp Gly Lys	1185
Cys Leu Pro Trp	1190	Ala Leu Gly Cys Arg	1195	Lys Lys Thr Pro Lys	1200
Lys Tyr Met Tyr	1205	Leu Ala Gln Glu Leu	1210	Val Val Asp Pro Glu	1215
Pro Pro Lys Pro	1220	Gln Thr Thr Thr Glu	1225	Ala Lys Ala Leu Val	1230
Glu Asn Gly Ser	1235	Cys Gln Ile Ile Thr	1240	Ile Thr	1245
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<213> Homo sapiens

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<223> Incyte ID No: 3046849CD1

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Phe Gly Tyr Asn Leu Ser Ile Ile Asn Ala Pro Thr Leu His Ile
 35      40      45
Gln Glu Phe Thr Asn Glu Thr Trp Gln Ala Arg Thr Gly Glu Pro
 50      55      60
Leu Pro Asp His Leu Val Leu Leu Met Trp Ser Leu Ile Val Ser
 65      70      75
Leu Tyr Pro Leu Gly Gly Leu Phe Gly Ala Leu Leu Ala Gly Pro
 80      85      90
Leu Ala Ile Thr Leu Gly Arg Lys Lys Ser Leu Leu Val Asn Asn
 95      100     105
Ile Phe Val Val Ser Ala Ala Ile Leu Phe Gly Phe Ser Arg Lys
 110     115     120
Ala Gly Ser Phe Glu Met Ile Met Leu Gly Arg Leu Leu Val Gly
 125     130     135
Val Asn Ala Gly Val Ser Met Asn Ile Gln Pro Met Tyr Leu Gly
 140     145     150
Glu Ser Ala Pro Lys Glu Leu Arg Gly Ala Val Ala Met Ser Ser
 155     160     165
Ala Ile Phe Thr Ala Leu Gly Ile Val Met Gly Gln Val Val Gly
 170     175     180
Leu Arg Glu Leu Leu Gly Gly Pro Gln Ala Trp Pro Leu Leu Leu
 185     190     195
Ala Ser Cys Leu Val Pro Gly Ala Leu Gln Leu Ala Ser Leu Pro
 200     205     210
Leu Leu Pro Glu Ser Pro Arg Tyr Leu Leu Ile Asp Cys Gly Asp
 215     220     225
Thr Glu Ala Cys Leu Ala Ala Leu Arg Gln Leu Arg Gly Ser Gly
 230     235     240
Asp Leu Ala Gly Glu Leu Glu Glu Leu Glu Glu Arg Ala Ala
 245     250     255
Cys Gln Gly Cys Arg Ala Arg Arg Pro Trp Glu Leu Phe Gln His
 260     265     270
Arg Ala Leu Arg Arg Gln Val Thr Ser Leu Val Val Leu Gly Ser
 275     280     285
Ala Met Glu Leu Cys Gly Asn Asp Ser Val Tyr Ala Tyr Ala Ser
 290     295     300
Ser Val Phe Arg Lys Ala Gly Val Pro Glu Ala Lys Ile Gln Tyr
 305     310     315
Ala Ile Ile Gly Thr Gly Ser Cys Glu Leu Leu Thr Ala Val Val
 320     325     330
Ser Cys Val Val Ile Glu Arg Val Gly Arg Arg Val Leu Leu Ile
 335     340     345
Gly Gly Tyr Ser Leu Met Thr Cys Trp Gly Ser Ile Phe Thr Val
 350     355     360
Ala Leu Cys Leu Gln Ser Ser Phe Pro Trp Thr Leu Tyr Leu Ala
 365     370     375
Met Ala Cys Ile Phe Ala Phe Ile Leu Ser Phe Gly Ile Gly Pro
 380     385     390
Ala Gly Val Thr Gly Ile Leu Ala Thr Glu Leu Phe Asp Gln Met
 395     400     405
Ala Arg Pro Ala Ala Cys Met Val Cys Gly Ala Leu Met Trp Ile
 410     415     420
Met Leu Ile Leu Val Gly Leu Gly Phe Pro Phe Ile Met Glu Ala
 425     430     435
Leu Ser His Phe Leu Tyr Val Pro Phe Leu Gly Val Cys Val Cys
 440     445     450
Gly Ala Ile Tyr Thr Gly Leu Phe Leu Pro Glu Thr Lys Gly Lys
 455     460     465
Thr Phe Gln Glu Ile Ser Lys Glu Leu His Arg Leu Asn Phe Pro
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Arg Arg Ala Gln Gly Pro Thr Trp Arg Ser Leu Glu Val Ile Gln
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Ser Thr Glu Leu

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 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Incyte ID No: 4538363CD1

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 20 25 30
 Asn Val Ala Val Gly Ile Trp Ser Ser Cys Arg Ala Ser Arg Asn
 35 40 45
 Thr Val Asn Gly Tyr Phe Leu Ala Gly Arg Asp Met Thr Trp Trp
 50 55 60
 Pro Ile Gly Ala Ser Leu Phe Ala Ser Ser Glu Gly Ser Gly Leu
 65 70 75
 Phe Ile Gly Leu Ala Gly Ser Gly Ala Ala Gly Gly Leu Ala Val
 80 85 90
 Ala Gly Phe Glu Trp Asn Ala Thr Tyr Val Leu Leu Ala Leu Ala
 95 100 105
 Trp Val Phe Val Pro Ile Tyr Ile Ser Ser Glu Ile Val Thr Leu
 110 115 120
 Pro Glu Tyr Ile Gln Lys Arg Tyr Gly Gly Gln Arg Ile Arg Met
 125 130 135
 Tyr Leu Ser Val Leu Ser Leu Leu Leu Ser Val Phe Thr Lys Ile
 140 145 150
 Ser Leu Asp Leu Tyr Ala Gly Ala Leu Phe Val His Ile Cys Leu
 155 160 165
 Gly Trp Asn Phe Tyr Leu Ser Thr Ile Leu Thr Leu Gly Ile Thr
 170 175 180
 Ala Leu Tyr Thr Ile Ala Gly Gly Leu Ala Ala Val Ile Tyr Thr
 185 190 195
 Asp Ala Leu Gln Thr Leu Ile Met Val Val Gly Ala Val Ile Leu
 200 205 210
 Thr Ile Lys Ala Phe Asp Gln Ile Gly Gly Tyr Gly Gln Leu Glu
 215 220 225
 Ala Ala Tyr Ala Gln Ala Ile Pro Ser Arg Thr Ile Ala Asn Thr
 230 235 240
 Thr Cys His Leu Pro Arg Thr Asp Ala Met His Met Phe Arg Asp
 245 250 255
 Pro His Thr Gly Asp Leu Pro Trp Thr Gly Met Thr Phe Gly Leu
 260 265 270
 Thr Ile Met Ala Thr Trp Tyr Trp Cys Thr Asp Gln Val Ile Val
 275 280 285
 Gln Arg Ser Leu Ser Ala Arg Asp Leu Asn His Ala Lys Ala Gly
 290 295 300
 Ser Ile Leu Ala Ser Tyr Leu Lys Met Leu Pro Met Gly Leu Ile
 305 310 315
 Ile Met Pro Gly Met Ile Ser Arg Ala Leu Phe Pro Asp Asp Val
 320 325 330
 Gly Cys Val Val Pro Ser Glu Cys Leu Arg Ala Cys Gly Ala Glu
 335 340 345
 Val Gly Cys Ser Asn Ile Ala Tyr Pro Lys Leu Val Met Glu Leu
 350 355 360
 Met Pro Ile Gly Leu Arg Gly Leu Met Ile Ala Val Met Leu Ala
 365 370 375
 Ala Leu Met Ser Ser Leu Thr Ser Ile Phe Asn Ser Ser Ser Thr
 380 385 390
 Leu Phe Thr Met Asp Ile Trp Arg Arg Leu Arg Pro Arg Ser Gly
 395 400 405

Glu Arg Glu Leu	Leu Leu Val Gly Arg	Leu Val Ile Val Ala	Leu
410	415		420
Ile Gly Val Ser	Val Ala Trp Ile Pro	Val Leu Gln Asp Ser	Asn
425	430		435
Ser Gly Gln Leu	Phe Ile Tyr Met Gln	Ser Val Thr Ser Ser	Leu
440	445		450
Ala Pro Pro Val	Thr Ala Val Phe Val	Leu Gly Val Phe Trp	Arg
455	460		465
Arg Ala Asn Glu	Gln Gly Ala Phe Trp	Gly Leu Ile Ala Gly	Leu
470	475		480
Val Val Gly Ala	Thr Arg Leu Val Leu	Glu Phe Leu Asn Pro	Ala
485	490		495
Pro Pro Cys Gly	Glu Pro Asp Thr Arg	Pro Ala Val Leu Gly	Ser
500	505		510
Ile His Tyr Leu	His Phe Ala Val Ala	Leu Phe Ala Leu Ser	Gly
515	520		525
Ala Val Val Val	Ala Gly Ser Leu Leu	Thr Pro Pro Pro Gln	Ser
530	535		540
Val Gln Ile Glu	Asn Leu Thr Trp Trp	Thr Leu Ala Gln Asp	Val
545	550		555
Pro Leu Gly Thr	Lys Ala Gly Asp Gly	Gln Thr Pro Gln Lys	His
560	565		570
Ala Phe Trp Ala	Arg Val Cys Gly Phe	Asn Ala Ile Leu Leu	Met
575	580		585
Cys Val Asn Ile	Phe Phe Tyr Ala Tyr	Phe Ala	
590	595		

<210> 17

<211> 1192

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 6427460CD1

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Gly Glu Glu Asn	Trp Val Asp Ser Arg	Thr Ile Tyr Val Gly	His
20	25		30
Arg Glu Pro Pro	Pro Gly Ala Glu Ala	Tyr Ile Pro Gln Arg	Tyr
35	40		45
Pro Asp Asn Arg	Ile Val Ser Ser Lys	Tyr Thr Phe Trp Asn	Phe
50	55		60
Ile Pro Lys Asn	Leu Phe Glu Gln Phe	Arg Arg Val Ala Asn	Phe
65	70		75
Tyr Phe Leu Ile	Ile Phe Leu Val Gln	Leu Ile Ile Asp Thr	Pro
80	85		90
Thr Ser Pro Val	Thr Ser Gly Leu Pro	Leu Phe Phe Val Ile	Thr
95	100		105
Val Thr Ala Ile	Lys Gln Gly Tyr Glu	Asp Trp Leu Arg His	Lys
110	115		120
Ala Asp Asn Ala	Met Asn Gln Cys Pro	Val His Phe Ile Gln	His
125	130		135
Gly Lys Leu Val	Arg Lys Gln Ser Arg	Lys Leu Arg Val Gly	Asp
140	145		150
Ile Val Met Val	Lys Glu Asp Glu Thr	Phe Pro Cys Asp Leu	Ile
155	160		165
Phe Leu Ser Ser	Asn Arg Gly Asp Gly	Thr Cys His Val Thr	Thr
170	175		180
Ala Ser Leu Asp	Gly Glu Ser Ser His	Lys Thr His Tyr Ala	Val
185	190		195
Gln Asp Thr Lys	Gly Phe His Thr Glu	Glu Asp Ile Gly Gly	Leu
200	205		210
His Ala Thr Ile	Glu Cys Glu Gln Pro	Gln Pro Asp Leu Tyr	Lys
215	220		225

Phe	Val	Gly	Arg	Ile	Asn	Val	Tyr	Ser	Asp	Leu	Asn	Asp	Pro	Val	
				230					235					240	
Val	Arg	Pro	Leu	Gly	Ser	Glu	Asn	Leu	Leu	Leu	Arg	Gly	Ala	Thr	
				245					250					255	
Leu	Lys	Asn	Thr	Glu	Lys	Ile	Phe	Gly	Val	Ala	Ile	Tyr	Thr	Gly	
				260					265					270	
Met	Glu	Thr	Lys	Met	Ala	Leu	Asn	Tyr	Gln	Ser	Lys	Ser	Gln	Lys	
				275					280					285	
Arg	Ser	Ala	Val	Glu	Lys	Ser	Met	Asn	Ala	Phe	Leu	Ile	Val	Tyr	
				290					295					300	
Leu	Cys	Ile	Leu	Ile	Ser	Lys	Ala	Leu	Ile	Asn	Thr	Val	Leu	Lys	
				305					310					315	
Tyr	Val	Trp	Gln	Ser	Glu	Pro	Phe	Arg	Asp	Glu	Pro	Trp	Tyr	Asn	
				320					325					330	
Gln	Lys	Thr	Glu	Ser	Glu	Arg	Gln	Arg	Asn	Leu	Phe	Leu	Lys	Ala	
				335					340					345	
Phe	Thr	Asp	Phe	Leu	Ala	Phe	Met	Val	Leu	Phe	Asn	Tyr	Ile	Ile	
				350					355					360	
Pro	Val	Ser	Met	Tyr	Val	Thr	Val	Glu	Met	Gln	Lys	Phe	Leu	Gly	
				365					370					375	
Ser	Tyr	Phe	Ile	Thr	Trp	Asp	Glu	Asp	Met	Phe	Asp	Glu	Glu	Thr	
				380					385					390	
Gly	Glu	Gly	Pro	Leu	Val	Asn	Thr	Ser	Asp	Leu	Asn	Glu	Glu	Leu	
				395					400					405	
Gly	Gln	Val	Glu	Tyr	Ile	Phe	Thr	Asp	Lys	Thr	Gly	Thr	Leu	Thr	
				410					415					420	
Glu	Asn	Asn	Met	Glu	Phe	Lys	Glu	Cys	Cys	Ile	Glu	Gly	His	Val	
				425					430					435	
Tyr	Val	Pro	His	Val	Ile	Cys	Asn	Gly	Gln	Val	Leu	Pro	Glu	Ser	
				440					445					450	
Ser	Gly	Ile	Asp	Met	Ile	Asp	Ser	Ser	Pro	Ser	Val	Asn	Gly	Arg	
				455					460					465	
Glu	Arg	Glu	Glu	Leu	Phe	Phe	Arg	Ala	Leu	Cys	Leu	Cys	His	Thr	
				470					475					480	
Val	Gln	Val	Lys	Asp	Asp	Asp	Ser	Val	Asp	Gly	Pro	Arg	Lys	Ser	
				485					490					495	
Pro	Asp	Gly	Gly	Lys	Ser	Cys	Val	Tyr	Ile	Ser	Ser	Ser	Pro	Asp	
				500					505					510	
Glu	Val	Ala	Leu	Val	Glu	Gly	Val	Gln	Arg	Leu	Gly	Phe	Thr	Tyr	
				515					520					525	
Leu	Arg	Leu	Lys	Asp	Asn	Tyr	Met	Glu	Ile	Leu	Asn	Arg	Glu	Asn	
				530					535					540	
His	Ile	Glu	Arg	Phe	Glu	Leu	Leu	Glu	Ile	Leu	Ser	Phe	Asp	Ser	
				545					550					555	
Val	Arg	Arg	Arg	Met	Ser	Val	Ile	Val	Lys	Ser	Ala	Thr	Gly	Glu	
				560					565					570	
Ile	Tyr	Leu	Phe	Cys	Lys	Gly	Ala	Asp	Ser	Ser	Ile	Phe	Pro	Arg	
				575					580					585	
Val	Ile	Glu	Gly	Lys	Val	Asp	Gln	Ile	Arg	Ala	Arg	Val	Glu	Arg	
				590					595					600	
Asn	Ala	Val	Glu	Gly	Leu	Arg	Thr	Leu	Cys	Val	Ala	Tyr	Lys	Arg	
				605					610					615	
Leu	Ile	Gln	Glu	Glu	Tyr	Glu	Gly	Ile	Cys	Lys	Leu	Leu	Gln	Ala	
				620					625					630	
Ala	Lys	Val	Ala	Leu	Gln	Asp	Arg	Glu	Lys	Lys	Leu	Ala	Glu	Ala	
				635					640					645	
Tyr	Glu	Gln	Ile	Glu	Lys	Asp	Leu	Thr	Leu	Leu	Gly	Ala	Thr	Ala	
				650					655					660	
Val	Glu	Asp	Arg	Leu	Gln	Glu	Lys	Ala	Ala	Asp	Thr	Ile	Glu	Ala	
				665					670					675	
Leu	Gln	Lys	Ala	Gly	Ile	Lys	Val	Trp	Val	Leu	Thr	Gly	Asp	Lys	
				680					685					690	
Met	Glu	Thr	Ala	Ala	Ala	Thr	Cys	Tyr	Ala	Cys	Lys	Leu	Phe	Arg	
				695					700					705	
Arg	Asn	Thr	Gln	Leu	Leu	Glu	Leu	Thr	Thr	Lys	Arg	Ile	Glu	Glu	
				710					715					720	
Gln	Ser	Leu	His	Asp	Val	Leu	Phe	Glu	Leu	Ser	Lys	Thr	Val	Leu	

Arg His Ser Gly	725	Leu Thr Arg Asp	730	Leu Ser Gly Leu	735
Ala Asp Met Gln	740	Asn Ile Ile Asp	745	Gly Ala Ala Leu	750
Ser Leu Ile Met	755	Gly Pro Arg Glu	760	Asn Tyr	765
Arg Glu Leu Phe	770	Leu Glu Ile Cys	775	Ser Ser Gly	780
Cys Cys Arg Met	785	Ala Pro Leu Gln	790	Ser Cys Ser	795
Ile Lys Phe Ser	800	Lys Thr Leu Ala	805	Ile Val Lys	810
Gly Ala Asn Asp	815	Glu His Pro Ile	820	Gly Asp	825
Gly Val Ile Gly	830	Val Ser Met Ile	835	Leu Ala His	840
Tyr Ala Ile Pro	845	Glu Gly Arg Gln	850	Val Gly Ile	855
His Gly His Phe	860	Lys Phe Lys His	865	Asn Ser	870
Phe Phe Tyr Lys	875	Leu Lys Lys Met	880	Leu Leu Val	885
Gln Phe Phe Cys	890	Tyr Tyr Ile Arg	895	Glu Leu Val	900
Tyr Leu Thr Leu	905	Asn Val Cys Phe	910	Gln Phe Leu	915
Leu Tyr Ser Leu	920	Gly Phe Ser Gln	925	Thr Ala	930
Arg Asp Pro Thr	935	Thr Asn Ile Ser	940	Leu Tyr Asp	945
Arg Trp Arg Val	950	Leu Tyr Arg Asp	955	Thr Leu Pro	960
Ala Leu Val Phe	965	Phe Ile Tyr Trp	970	Ile Asp Val	975
Thr Val Thr Ser	980	Ala Phe Gly Ala	985	Leu Leu Phe	990
Thr Leu Val Phe	995	Thr Phe Gly Ala	1000	Asn Thr	1005
Ala Leu Asp Thr	1010	Asn Gly Gln Ile	1015	Thr Thr Phe	1020
Trp Gly Ser Leu	1025	Val Met Val Phe	1030	Val Thr Leu	1035
Gly Val Ile Trp	1040	Thr Trp Thr Trp	1045	Lys Leu	1050
Phe Ile Gln Met	1055	Val Phe Val Val	1060	Trp Leu	1065
Leu Leu Val Thr	1070	Pro Phe Leu Asn	1075	Ala Ile Val	1080
Leu Cys Arg Gln	1085	Tyr Ser Ser Gly	1090	Thr Tyr Val	1095
Asn Gly Cys Ala	1100	Leu Ser Ser Gly	1105	Arg Met Tyr	1110
Leu Ala Ser Leu	1115	Pro Trp Pro Thr	1120	Val Thr Leu	1125
Ala Ala Trp Tyr	1130	Ala Thr Glu Arg	1135	Val Gln Gln	1140
Trp Lys Glu Lys	1145	Val Ser His Ser	1150	Val Thr Leu	1155
Ser His His His	1160	Gln Val Thr Leu	1165	Ala Ala	1170
Ser Arg Val Gly	1175	Val Ser Thr Glu	1180	Gly Gly	1185
	1190	Pro Pro Ile Leu			
		Pro Ser His Ser			
		Cys Pro Arg			
		Met Leu Val			

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 <212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474127CD1

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Gly	Thr	Arg	His	Glu	Thr	Tyr	Arg	Ser	Thr	Leu	Lys	Thr	Leu	Pro	20	25	30	35
Gly	Thr	Arg	Leu	Ala	Leu	Leu	Ala	Ser	Ser	Glu	Pro	Pro	Gly	Asp	40	45	50	55
Cys	Leu	Thr	Thr	Ala	Gly	Asp	Lys	Leu	Gln	Pro	Ser	Pro	Pro	Pro	60	65	70	75
Leu	Ser	Pro	Pro	Pro	Arg	Ala	Pro	Pro	Leu	Ser	Pro	Gly	Pro	Gly	80	85	90	95
Gly	Cys	Phe	Glu	Gly	Gly	Ala	Gly	Asn	Cys	Ser	Ser	Arg	Gly	Gly	100	105	110	115
Arg	Ala	Ser	Asp	His	Pro	Gly	Gly	Gly	Arg	Glu	Phe	Phe	Phe	Asp	120	125	130	135
Arg	His	Pro	Gly	Val	Phe	Ala	Tyr	Val	Leu	Asn	Tyr	Tyr	Arg	Thr	140	145	150	155
Gly	Lys	Leu	His	Cys	Pro	Ala	Asp	Val	Cys	Gly	Pro	Leu	Phe	Glu	160	165	170	175
Glu	Glu	Leu	Ala	Phe	Trp	Gly	Ile	Asp	Glu	Thr	Asp	Val	Glu	Pro	180	185	190	195
Cys	Cys	Trp	Met	Thr	Tyr	Arg	Gln	His	Arg	Asp	Ala	Glu	Glu	Ala	200	205	210	215
Leu	Asp	Ile	Phe	Glu	Thr	Pro	Asp	Leu	Ile	Gly	Gly	Asp	Pro	Gly	220	225	230	235
Asp	Asp	Glu	Asp	Leu	Ala	Ala	Lys	Arg	Leu	Gly	Ile	Glu	Asp	Ala	240	245	250	255
Ala	Gly	Leu	Gly	Gly	Pro	Asp	Gly	Lys	Ser	Gly	Arg	Trp	Arg	Arg	260	265	270	275
Leu	Gln	Pro	Arg	Met	Trp	Ala	Leu	Phe	Glu	Asp	Pro	Tyr	Ser	Ser	280	285	290	295
Arg	Ala	Ala	Arg	Phe	Ile	Ala	Phe	Ala	Ser	Leu	Phe	Phe	Ile	Leu	300	305	310	315
Val	Ser	Ile	Thr	Thr	Phe	Cys	Leu	Glu	Thr	His	Glu	Ala	Phe	Asn	320	325	330	335
Ile	Val	Lys	Asn	Lys	Thr	Glu	Pro	Val	Ile	Asn	Gly	Thr	Ser	Val	340	345	350	355
Val	Leu	Gln	Tyr	Glu	Ile	Glu	Thr	Asp	Pro	Ala	Leu	Thr	Tyr	Val	360	365	370	375
Glu	Gly	Val	Cys	Val	Val	Trp	Phe	Thr	Phe	Glu	Phe	Leu	Val	Arg	380	385	390	395
Ile	Val	Phe	Ser	Pro	Asn	Lys	Leu	Glu	Phe	Ile	Lys	Asn	Leu	Leu	400	405	410	415
Asn	Ile	Ile	Asp	Phe	Val	Ala	Ile	Leu	Pro	Phe	Tyr	Leu	Glu	Val	420	425	430	435
Gly	Leu	Ser	Gly	Leu	Ser	Ser	Lys	Ala	Ala	Lys	Asp	Val	Leu	Gly	440	445	450	
Phe	Leu	Arg	Val	Val	Arg	Phe	Val	Arg	Ile	Leu	Arg	Ile	Phe	Lys				
Leu	Thr	Arg	His	Phe	Val	Gly	Leu	Arg	Val	Leu	Gly	His	Thr	Leu				
Arg	Ala	Ser	Thr	Asn	Glu	Phe	Leu	Leu	Leu	Ile	Ile	Phe	Leu	Ala				
Leu	Gly	Val	Leu	Ile	Phe	Ala	Thr	Met	Ile	Tyr	Tyr	Ala	Glu	Arg				
Val	Gly	Ala	Gln	Pro	Asn	Asp	Pro	Ser	Ala	Ser	Glu	His	Thr	Gln				
Phe	Lys	Asn	Ile	Pro	Ile	Gly	Phe	Trp	Trp	Ala	Val	Val	Thr	Met				
Thr	Thr	Leu	Gly	Tyr	Gly	Asp	Met	Tyr	Pro	Gln	Thr	Trp	Ser	Gly				

Met	Leu	Val	Gly	Ala	Leu	Cys	Ala	Leu	Ala	Gly	Val	Leu	Thr	Ile	
				455					460					465	
Ala	Met	Pro	Val	Pro	Val	Ile	Val	Asn	Asn	Phe	Gly	Met	Tyr	Tyr	
				470					475					480	
Ser	Leu	Ala	Met	Ala	Lys	Gln	Lys	Leu	Pro	Arg	Lys	Arg	Lys	Lys	
				485					490					495	
His	Ile	Pro	Pro	Ala	Pro	Gln	Ala	Ser	Ser	Pro	Thr	Phe	Cys	Lys	
				500					505					510	
Thr	Glu	Leu	Asn	Met	Ala	Cys	Asn	Ser	Thr	Gln	Ser	Asp	Thr	Cys	
				515					520					525	
Leu	Gly	Lys	Asp	Asn	Arg	Leu	Leu	Glu	His	Asn	Arg	Ser	Val	Leu	
				530					535					540	
Ser	Gly	Asp	Asp	Ser	Thr	Gly	Ser	Glu	Pro	Pro	Leu	Ser	Pro	Pro	
				545					550					555	
Glu	Arg	Leu	Pro	Ile	Arg	Arg	Ser	Ser	Thr	Arg	Asp	Lys	Asn	Arg	
				560					565					570	
Arg	Gly	Glu	Thr	Cys	Phe	Leu	Leu	Thr	Thr	Gly	Asp	Tyr	Thr	Cys	
				575					580					585	
Ala	Ser	Asp	Gly	Gly	Ile	Arg	Lys	Gly	Tyr	Glu	Lys	Ser	Arg	Ser	
				590					595					600	
Leu	Asn	Asn	Ile	Ala	Gly	Leu	Ala	Gly	Asn	Ala	Leu	Arg	Leu	Ser	
				605					610					615	
Pro	Val	Thr	Ser	Pro	Tyr	Asn	Ser	Pro	Cys	Pro	Leu	Arg	Arg	Ser	
				620					625					630	
Arg	Ser	Pro	Ile	Pro	Ser	Ile	Leu								
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<211> 681

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7476949CD1

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Met	Ser	Lys	Asp	Leu	Ala	Ala	Met	Gly	Pro	Gly	Ala	Ser	Gly	Asp	
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Gly	Val	Arg	Thr	Glu	Thr	Ala	Pro	His	Ile	Ala	Leu	Asp	Ser	Arg	
				20					25					30	
Val	Gly	Leu	His	Ala	Tyr	Asp	Ile	Ser	Val	Val	Val	Ile	Tyr	Phe	
				35					40					45	
Val	Phe	Val	Ile	Ala	Val	Gly	Ile	Trp	Ser	Ser	Ile	Arg	Ala	Ser	
				50					55					60	
Arg	Gly	Thr	Ile	Gly	Gly	Tyr	Phe	Leu	Ala	Gly	Arg	Ser	Met	Ser	
				65					70					75	
Trp	Trp	Pro	Ile	Gly	Ala	Ser	Leu	Met	Ser	Ser	Asn	Val	Gly	Ser	
				80					85					90	
Gly	Leu	Phe	Ile	Gly	Leu	Ala	Gly	Thr	Gly	Ala	Ala	Gly	Gly	Leu	
				95					100					105	
Ala	Val	Gly	Gly	Phe	Glu	Trp	Asn	Ala	Thr	Trp	Leu	Leu	Leu	Ala	
				110					115					120	
Leu	Gly	Trp	Val	Phe	Val	Pro	Val	Tyr	Ile	Ala	Ala	Gly	Val	Val	
				125					130					135	
Thr	Met	Pro	Gln	Tyr	Leu	Lys	Lys	Arg	Phe	Gly	Gly	Gln	Arg	Ile	
				140					145					150	
Gln	Val	Tyr	Met	Ser	Val	Leu	Ser	Leu	Ile	Leu	Tyr	Ile	Phe	Thr	
				155					160					165	
Lys	Ile	Ser	Thr	Asp	Ile	Phe	Ser	Gly	Ala	Leu	Phe	Ile	Gln	Met	
				170					175					180	
Ala	Leu	Gly	Trp	Asn	Leu	Tyr	Leu	Ser	Thr	Gly	Ile	Leu	Leu	Val	
				185					190					195	
Val	Thr	Ala	Val	Thr	Ile	Ala	Gly	Gly	Leu	Met	Ala	Val	Ile		
				200					205					210	
Tyr	Thr	Asp	Ala	Leu	Gln	Thr	Val	Ile	Met	Val	Gly	Gly	Ala	Leu	
				215					220					225	

Val	Leu	Met	Phe	Leu	Gly	Phe	Gln	Asp	Val	Gly	Trp	Tyr	Pro	Gly	
				230					235					240	
Leu	Glu	Gln	Arg	Tyr	Arg	Gln	Ala	Ile	Pro	Asn	Val	Thr	Val	Pro	
				245					250					255	
Asn	Thr	Thr	Cys	His	Leu	Pro	Arg	Pro	Asp	Ala	Phe	His	Ile	Leu	
				260					265					270	
Arg	Asp	Pro	Val	Ser	Gly	Asp	Ile	Pro	Trp	Pro	Gly	Leu	Ile	Phe	
				275					280					285	
Gly	Leu	Thr	Val	Leu	Ala	Thr	Trp	Cys	Trp	Cys	Thr	Asp	Gln	Val	
				290					295					300	
Ile	Val	Gln	Arg	Ser	Leu	Ser	Ala	Lys	Ser	Leu	Ser	His	Ala	Lys	
				305					310					315	
Gly	Gly	Ser	Val	Leu	Gly	Gly	Tyr	Leu	Lys	Ile	Leu	Pro	Met	Phe	
				320					325					330	
Phe	Ile	Val	Met	Pro	Gly	Met	Ile	Ser	Arg	Ala	Leu	Phe	Pro	Asp	
				335					340					345	
Glu	Val	Gly	Cys	Val	Asp	Pro	Asp	Val	Cys	Gln	Arg	Ile	Cys	Gly	
				350					355					360	
Ala	Arg	Val	Gly	Cys	Ser	Asn	Ile	Ala	Tyr	Pro	Lys	Leu	Val	Met	
				365					370					375	
Ala	Leu	Met	Pro	Val	Gly	Leu	Arg	Gly	Leu	Met	Ile	Ala	Val	Ile	
				380					385					390	
Met	Ala	Ala	Leu	Met	Ser	Ser	Leu	Thr	Ser	Ile	Phe	Asn	Ser	Ser	
				395					400					405	
Ser	Thr	Leu	Phe	Thr	Ile	Asp	Val	Trp	Gln	Arg	Phe	Arg	Arg	Lys	
				410					415					420	
Ser	Thr	Glu	Gln	Glu	Leu	Met	Val	Val	Gly	Arg	Val	Phe	Val	Val	
				425					430					435	
Phe	Leu	Val	Val	Ile	Ser	Ile	Leu	Trp	Ile	Pro	Ile	Ile	Gln	Ser	
				440					445					450	
Ser	Asn	Ser	Gly	Gln	Leu	Phe	Asp	Tyr	Ile	Gln	Ala	Val	Thr	Ser	
				455					460					465	
Tyr	Leu	Ala	Pro	Pro	Ile	Thr	Ala	Leu	Phe	Leu	Leu	Ala	Ile	Phe	
				470					475					480	
Cys	Lys	Arg	Val	Thr	Glu	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Val	Phe	
				485					490					495	
Gly	Leu	Gly	Val	Gly	Leu	Leu	Arg	Met	Ile	Leu	Glu	Phe	Ser	Tyr	
				500					505					510	
Pro	Ala	Pro	Ala	Cys	Gly	Glu	Val	Asp	Arg	Arg	Pro	Ala	Val	Leu	
				515					520					525	
Lys	Asp	Phe	His	Tyr	Leu	Tyr	Phe	Ala	Ile	Leu	Leu	Cys	Gly	Leu	
				530					535					540	
Thr	Ala	Ile	Val	Ile	Val	Ile	Val	Ser	Leu	Cys	Thr	Thr	Pro	Ile	
				545					550					555	
Pro	Glu	Glu	Gln	Leu	Thr	Arg	Leu	Thr	Trp	Trp	Thr	Arg	Asn	Cys	
				560					565					570	
Pro	Leu	Ser	Glu	Leu	Glu	Lys	Glu	Ala	His	Glu	Ser	Thr	Pro	Glu	
				575					580					585	
Ile	Ser	Glu	Arg	Pro	Ala	Gly	Glu	Cys	Pro	Ala	Gly	Gly	Gly	Ala	
				590					595					600	
Ala	Glu	Asn	Ser	Ser	Leu	Gly	Gln	Glu	Gln	Pro	Glu	Ala	Pro	Ser	
				605					610					615	
Arg	Ser	Trp	Gly	Lys	Leu	Leu	Trp	Ser	Trp	Phe	Cys	Gly	Leu	Ser	
				620					625					630	
Gly	Thr	Pro	Glu	Gln	Ala	Leu	Ser	Pro	Ala	Glu	Lys	Ala	Ala	Leu	
				635					640					645	
Glu	Gln	Lys	Leu	Thr	Ser	Ile	Glu	Glu	Glu	Pro	Leu	Trp	Arg	His	
				650					655					660	
Val	Cys	Asn	Ile	Asn	Ala	Val	Leu	Leu	Leu	Ala	Ile	Asn	Ile	Phe	
				665					670					675	
Leu	Trp	Gly	Tyr	Phe	Ala										
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<211> 1096

<212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 7477249CD1

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Met	Trp	Arg	Trp	Ile	Arg	Gln	Gln	Leu	Gly	Phe	Asp	Pro	Pro	His
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Gln	Ser	Asp	Thr	Arg	Thr	Ile	Tyr	Val	Ala	Asn	Arg	Phe	Pro	Gln
				20					25					30
Asn	Gly	Leu	Tyr	Thr	Pro	Gln	Lys	Phe	Ile	Asp	Asn	Arg	Ile	Ile
				35					40					45
Ser	Ser	Lys	Tyr	Thr	Val	Trp	Asn	Phe	Val	Pro	Lys	Asn	Leu	Phe
				50					55					60
Glu	Gln	Phe	Arg	Arg	Val	Ala	Asn	Phe	Tyr	Phe	Leu	Ile	Ile	Phe
				65					70					75
Leu	Val	Gln	Leu	Met	Ile	Asp	Thr	Pro	Thr	Ser	Pro	Val	Thr	Ser
				80					85					90
Gly	Leu	Pro	Leu	Phe	Phe	Val	Ile	Thr	Val	Thr	Ala	Ile	Lys	Gln
				95					100					105
Gly	Tyr	Glu	Asp	Trp	Leu	Arg	His	Asn	Ser	Asp	Asn	Glu	Val	Asn
				110					115					120
Gly	Ala	Pro	Val	Tyr	Val	Val	Arg	Ser	Gly	Gly	Leu	Val	Lys	Thr
				125					130					135
Arg	Ser	Lys	Asn	Ile	Arg	Val	Gly	Asp	Ile	Val	Arg	Ile	Ala	Lys
				140					145					150
Asp	Glu	Ile	Phe	Pro	Ala	Asp	Leu	Val	Leu	Leu	Ser	Ser	Asp	Arg
				155					160					165
Leu	Asp	Gly	Ser	Cys	His	Val	Thr	Thr	Ala	Ser	Leu	Asp	Gly	Glu
				170					175					180
Thr	Asn	Leu	Lys	Thr	His	Val	Ala	Val	Pro	Glu	Thr	Ala	Leu	Leu
				185					190					195
Gln	Thr	Val	Ala	Asn	Leu	Asp	Thr	Leu	Val	Ala	Val	Ile	Glu	Cys
				200					205					210
Gln	Gln	Pro	Glu	Ala	Asp	Leu	Tyr	Arg	Phe	Met	Gly	Arg	Met	Ile
				215					220					225
Ile	Thr	Gln	Gln	Met	Glu	Glu	Ile	Val	Arg	Pro	Leu	Gly	Pro	Glu
				230					235					240
Ser	Leu	Leu	Leu	Arg	Gly	Ala	Arg	Leu	Lys	Asn	Thr	Lys	Glu	Ile
				245					250					255
Phe	Gly	Val	Ala	Val	Tyr	Thr	Gly	Met	Glu	Thr	Lys	Met	Ala	Leu
				260					265					270
Asn	Tyr	Lys	Ser	Lys	Ser	Gln	Lys	Arg	Ser	Ala	Val	Glu	Lys	Ser
				275					280					285
Met	Asn	Thr	Phe	Leu	Ile	Ile	Tyr	Leu	Val	Ile	Leu	Ile	Ser	Glu
				290					295					300
Ala	Val	Ile	Ser	Thr	Ile	Leu	Lys	Tyr	Thr	Trp	Gln	Ala	Glu	Glu
				305					310					315
Lys	Trp	Asp	Glu	Pro	Trp	Tyr	Asn	Gln	Lys	Thr	Glu	His	Gln	Arg
				320					325					330
Asn	Ser	Ser	Lys	Val	Glu	Tyr	Val	Phe	Thr	Asp	Lys	Thr	Gly	Thr
				335					340					345
Leu	Thr	Glu	Asn	Glu	Met	Gln	Phe	Arg	Glu	Cys	Ser	Ile	Asn	Gly
				350					355					360
Met	Lys	Tyr	Gln	Glu	Ile	Asn	Gly	Arg	Leu	Val	Pro	Glu	Gly	Pro
				365					370					375
Thr	Pro	Asp	Ser	Ser	Glu	Gly	Asn	Leu	Ser	Tyr	Leu	Ser	Ser	Leu
				380					385					390
Ser	His	Leu	Asn	Asn	Leu	Ser	His	Leu	Thr	Thr	Ser	Ser	Ser	Phe
				395					400					405
Arg	Thr	Ser	Pro	Glu	Asn	Glu	Thr	Glu	Leu	Ile	Lys	Glu	His	Asp
				410					415					420
Leu	Phe	Phe	Lys	Ala	Val	Ser	Leu	Cys	His	Thr	Val	Gln	Ile	Ser
				425					430					435
Asn	Val	Gln	Thr	Asp	Cys	Thr	Gly	Asp	Gly	Pro	Trp	Gln	Ser	Asn
				440					445					450
Leu	Ala	Pro	Ser	Gln	Leu	Glu	Tyr	Tyr	Ala	Ser	Ser	Pro	Asp	Glu
				455					460					465

Lys	Ala	Leu	Val	Glu	Ala	Ala	Ala	Arg	Ile	Gly	Ile	Val	Phe	Ile
				470					475					480
Gly	Asn	Ser	Glu	Glu	Thr	Met	Glu	Val	Lys	Thr	Leu	Gly	Lys	Leu
				485					490					495
Glu	Arg	Tyr	Lys	Leu	Leu	His	Ile	Leu	Glu	Phe	Asp	Ser	Asp	Arg
				500					505					510
Arg	Arg	Met	Ser	Val	Ile	Val	Gln	Ala	Pro	Ser	Gly	Glu	Lys	Leu
				515					520					525
Leu	Phe	Ala	Lys	Gly	Ala	Glu	Ser	Ser	Ile	Leu	Pro	Lys	Cys	Ile
				530					535					540
Gly	Gly	Glu	Ile	Glu	Lys	Thr	Arg	Ile	His	Val	Asp	Glu	Phe	Ala
				545					550					555
Leu	Lys	Gly	Leu	Arg	Thr	Leu	Cys	Ile	Ala	Tyr	Arg	Lys	Phe	Thr
				560					565					570
Ser	Lys	Glu	Tyr	Glu	Glu	Ile	Asp	Lys	Arg	Ile	Phe	Glu	Ala	Arg
				575					580					585
Thr	Ala	Leu	Gln	Gln	Arg	Glu	Glu	Lys	Leu	Ala	Ala	Val	Phe	Gln
				590					595					600
Phe	Ile	Glu	Lys	Asp	Leu	Ile	Leu	Leu	Gly	Ala	Thr	Ala	Val	Glu
				605					610					615
Asp	Arg	Leu	Gln	Asp	Lys	Val	Arg	Glu	Thr	Ile	Glu	Ala	Leu	Arg
				620					625					630
Met	Ala	Gly	Ile	Lys	Val	Trp	Val	Leu	Thr	Gly	Asp	Lys	His	Glu
				635					640					645
Thr	Ala	Val	Ser	Val	Ser	Leu	Ser	Cys	Gly	His	Phe	His	Arg	Thr
				650					655					660
Met	Asn	Ile	Leu	Glu	Leu	Ile	Asn	Gln	Lys	Ser	Asp	Ser	Glu	Cys
				665					670					675
Ala	Glu	Gln	Leu	Arg	Gln	Leu	Ala	Arg	Arg	Ile	Thr	Glu	Asp	His
				680					685					690
Val	Ile	Gln	His	Gly	Leu	Val	Val	Asp	Gly	Thr	Ser	Leu	Ser	Leu
				695					700					705
Ala	Leu	Arg	Glu	His	Glu	Lys	Leu	Phe	Met	Glu	Val	Cys	Arg	Asn
				710					715					720
Cys	Ser	Ala	Val	Leu	Cys	Cys	Arg	Met	Ala	Pro	Leu	Gln	Lys	Ala
				725					730					735
Lys	Val	Ile	Arg	Leu	Ile	Lys	Ile	Ser	Pro	Glu	Lys	Pro	Ile	Thr
				740					745					750
Leu	Ala	Val	Gly	Asp	Gly	Ala	Asn	Asp	Val	Ser	Met	Ile	Gln	Glu
				755					760					765
Ala	His	Val	Gly	Ile	Gly	Ile	Met	Gly	Lys	Glu	Gly	Arg	Gln	Ala
				770					775					780
Ala	Arg	Asn	Ser	Asp	Tyr	Ala	Ile	Ala	Arg	Phe	Lys	Phe	Leu	Ser
				785					790					795
Lys	Leu	Leu	Phe	Val	His	Gly	His	Phe	Tyr	Tyr	Ile	Arg	Ile	Ala
				800					805					810
Thr	Leu	Val	Gln	Tyr	Phe	Phe	Tyr	Lys	Asn	Val	Cys	Phe	Ile	Thr
				815					820					825
Pro	Gln	Phe	Leu	Tyr	Gln	Phe	Tyr	Cys	Leu	Phe	Ser	Gln	Gln	Thr
				830					835					840
Leu	Tyr	Asp	Ser	Val	Tyr	Leu	Thr	Leu	Tyr	Asn	Ile	Cys	Phe	Thr
				845					850					855
Ser	Leu	Pro	Ile	Leu	Ile	Tyr	Ser	Leu	Leu	Glu	Gln	His	Val	Asp
				860					865					870
Pro	His	Val	Leu	Gln	Asn	Lys	Pro	Thr	Leu	Tyr	Arg	Asp	Ile	Ser
				875					880					885
Lys	Asn	Arg	Leu	Leu	Ser	Ile	Lys	Thr	Phe	Leu	Tyr	Trp	Thr	Ile
				890					895					900
Leu	Gly	Phe	Ser	His	Ala	Phe	Ile	Phe	Phe	Phe	Gly	Ser	Tyr	Leu
				905					910					915
Leu	Ile	Gly	Lys	Asp	Thr	Ser	Leu	Leu	Gly	Asn	Gly	Gln	Met	Phe
				920					925					930
Gly	Asn	Trp	Thr	Phe	Gly	Thr	Leu	Val	Phe	Thr	Val	Met	Val	Ile
				935					940					945
Thr	Val	Thr	Val	Lys	Met	Ala	Leu	Glu	Thr	His	Phe	Trp	Thr	Trp
				950					955					960
Ile	Asn	His	Leu	Val	Thr	Trp	Gly	Ser	Ile	Ile	Phe	Tyr	Phe	Val

Phe	Ser	Leu	Phe	965	Gly	Gly	Ile	Leu	970	Pro	Phe	Leu	Gly	Ser	975
			Tyr	980					985						990
Gln	Asn	Met	Tyr	995	Val	Phe	Ile	Gln	1000	Leu	Ser	Ser	Gly	Ser	1005
Ala	Trp	Phe	Ala	1010	Ile	Leu	Met	Val	1015	Thr	Cys	Leu	Phe	Leu	1020
Asp	Ile	Ile	Lys	1025	Val	Phe	Asp	Arg	1030	Leu	His	Pro	Thr	Ser	1035
Thr	Glu	Lys	Ala	1040	Leu	Thr	Glu	Thr	1045	Ala	Gly	Ile	Lys	Cys	1050
Leu	Asp	Ser	Met	1055	Cys	Cys	Phe	Pro	1060	Glu	Gly	Glu	Ala	Ala	1065
Ser	Val	Gly	Arg	1070	Met	Leu	Glu	Arg	1075	Val	Ile	Gly	Arg	Cys	1080
Thr	His	Ile	Ser	1085	Arg	Cys	Glu	Ile	1090	Ser	Leu	Ser	Ser	Leu	1095
Arg															

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<211> 707

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477720CD1

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Leu	Leu	Leu	Val	Ala	Leu	Glu	Cys	Ser	Glu	Ala	Ser	Ser	Asp	Leu	
				20					25					30	
Asn	Glu	Ser	Ala	Asn	Ser	Thr	Ala	Gln	Tyr	Ala	Ser	Asn	Ala	Trp	
				35					40					45	
Phe	Ala	Ala	Ala	Ser	Ser	Glu	Pro	Glu	Glu	Gly	Ile	Ser	Val	Phe	
				50					55					60	
Glu	Leu	Asp	Tyr	Asp	Tyr	Val	Gln	Ile	Pro	Tyr	Glu	Val	Thr	Leu	
				65					70					75	
Trp	Ile	Leu	Leu	Ala	Ser	Leu	Ala	Lys	Ile	Gly	Phe	His	Leu	Tyr	
				80					85					90	
His	Arg	Leu	Pro	Gly	Leu	Met	Pro	Glu	Ser	Cys	Leu	Leu	Ile	Leu	
				95					100					105	
Val	Gly	Ala	Leu	Val	Gly	Gly	Ile	Ile	Phe	Gly	Thr	Asp	His	Lys	
				110					115					120	
Ser	Pro	Pro	Val	Met	Asp	Ser	Ser	Ile	Tyr	Phe	Leu	Tyr	Leu	Leu	
				125					130					135	
Pro	Pro	Ile	Val	Leu	Glu	Gly	Gly	Tyr	Phe	Met	Pro	Thr	Arg	Pro	
				140					145					150	
Phe	Phe	Glu	Asn	Ile	Gly	Ser	Ile	Leu	Trp	Trp	Ala	Val	Leu	Gly	
				155					160					165	
Ala	Leu	Ile	Asn	Ala	Leu	Gly	Ile	Gly	Leu	Ser	Leu	Tyr	Leu	Ile	
				170					175					180	
Cys	Gln	Val	Lys	Ala	Phe	Gly	Leu	Gly	Asp	Val	Asn	Leu	Leu	Gln	
				185					190					195	
Asn	Leu	Leu	Phe	Gly	Ser	Leu	Ile	Ser	Ala	Val	Asp	Pro	Val	Ala	
				200					205					210	
Val	Leu	Ala	Val	Phe	Glu	Glu	Ala	Arg	Val	Asn	Glu	Gln	Leu	Tyr	
				215					220					225	
Met	Met	Ile	Phe	Gly	Glu	Ala	Leu	Leu	Asn	Asp	Gly	Ile	Thr	Val	
				230					235					240	
Val	Leu	Tyr	Asn	Met	Leu	Ile	Ala	Phe	Thr	Lys	Met	His	Lys	Phe	
				245					250					255	
Glu	Asp	Ile	Glu	Thr	Val	Asp	Ile	Leu	Ala	Gly	Cys	Ala	Arg	Phe	
				260					265					270	
Ile	Val	Val	Gly	Leu	Gly	Gly	Val	Leu	Phe	Gly	Ile	Val	Phe	Gly	

Phe	Ile	Ser	Ala	275	Phe	Ile	Thr	Arg	Phe	280	Thr	Gln	Asn	Ile	Ser	285
Ile	Glu	Pro	Leu	290	Val	Phe	Met	Phe	295	Ser	Tyr	Leu	Ser	Tyr	300	Ala
Ala	Ala	Glu	Thr	305	Tyr	Leu	Ser	Gly	310	Ile	Leu	Ala	Ile	Thr	315	Ala
Cys	Ala	Val	Thr	320	Met	Lys	Lys	Tyr	325	Glu	Gln	Asn	Val	Ser	330	Gln
Thr	Ser	Tyr	Thr	335	Thr	Ile	Lys	Tyr	340	Met	Lys	Met	Leu	Ser	345	Ser
Val	Ser	Glu	Thr	350	Leu	Ile	Phe	Ile	355	Met	Gly	Val	Ser	Thr	360	Val
Gly	Lys	Asn	His	365	Glu	Trp	Asn	Trp	370	Phe	Ile	Cys	Phe	Thr	375	Leu
Ala	Phe	Cys	Gln	380	Ile	Trp	Arg	Ala	385	Ser	Val	Phe	Ala	Leu	390	Phe
Tyr	Ile	Ser	Asn	395	Gln	Phe	Arg	Thr	400	Pro	Phe	Ser	Ile	Lys	405	Asp
Gln	Cys	Ile	Ile	410	Phe	Tyr	Ser	Gly	415	Arg	Gly	Ala	Gly	Ser	420	Phe
Ser	Leu	Ala	Phe	425	Leu	Pro	Leu	Ser	430	Leu	Phe	Pro	Arg	Lys	435	Lys
Met	Phe	Val	Thr	440	Ala	Thr	Leu	Val	445	Ile	Tyr	Phe	Thr	Val	450	Phe
Ile	Gln	Gly	Ile	455	Thr	Val	Gly	Pro	460	Val	Arg	Tyr	Leu	Asp	465	Val
Lys	Lys	Thr	Asn	470	Lys	Lys	Glu	Ser	475	Asn	Glu	Glu	Leu	His	480	Ile
Arg	Leu	Met	Asp	485	His	Leu	Lys	Ala	490	Ile	Glu	Asp	Val	Cys	495	Gly
His	Trp	Ser	His	500	Tyr	Gln	Val	Arg	505	Lys	Phe	Lys	Lys	Phe	510	Asp
His	Arg	Tyr	Leu	515	Arg	Lys	Ile	Leu	520	Arg	Lys	Asn	Leu	Pro	525	Lys
Ser	Ser	Ile	Val	530	Ser	Leu	Tyr	Lys	535	Leu	Glu	Met	Lys	Gln	540	Ala
Ile	Glu	Met	Val	545	Glu	Thr	Gly	Ile	550	Ser	Ser	Thr	Ala	Phe	555	Ser
Ile	Pro	His	Gln	560	Ala	Gln	Arg	Ile	565	Gly	Ile	Lys	Arg	Leu	570	Ser
Pro	Glu	Asp	Val	575	Glu	Ser	Ile	Arg	580	Ile	Leu	Thr	Ser	Asn	585	Met
Tyr	Gln	Val	Arg	590	Gln	Arg	Thr	Leu	595	Tyr	Asn	Lys	Tyr	Asn	600	Leu
Lys	Pro	Gln	Thr	605	Ser	Glu	Lys	Gln	610	Lys	Glu	Ile	Leu	Ile	615	Arg
Arg	Gln	Asn	Thr	620	Leu	Arg	Glu	Ser	625	Arg	Lys	Gly	His	Ser	630	Leu
Pro	Trp	Gly	Lys	635	Pro	Ala	Gly	Thr	640	Asn	Ile	Arg	Tyr	Leu	645	Ser
Tyr	Pro	Tyr	Gly	650	Asn	Pro	Gln	Ser	655	Gly	Arg	Asp	Thr	Arg	660	Ala
Ala	Gly	Phe	Ser	665	Gly	Lys	Leu	Pro	670	Trp	Leu	Leu	Cys	Cys	675	Phe
Ser	Val	Glu	Ser	680	Gly	Gly	Lys	Tyr	685	Gly	Val	Trp	Ala	Lys	690	Arg
Gln	His			695					700						705	

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 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature

<223> Incyte ID No: 7477852CD1

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Gln	Lys	Leu	Leu	Pro	Ser	Phe	Leu	Val	Arg	Glu	Gln	Asp	Trp	Asp	
				20					25					30	
Gln	His	Leu	Asp	Lys	Leu	His	Met	Leu	Gln	Gln	Lys	Arg	Ile	Leu	
				35					40					45	
Glu	Ser	Pro	Leu	Leu	Arg	Ala	Ser	Lys	Glu	Asn	Asp	Leu	Ser	Val	
				50					55					60	
Leu	Arg	Gln	Leu	Leu	Leu	Asp	Cys	Thr	Cys	Asp	Val	Arg	Gln	Arg	
				65					70					75	
Gly	Ala	Leu	Gly	Glu	Thr	Ala	Leu	His	Ile	Ala	Ala	Leu	Tyr	Asp	
				80					85					90	
Asn	Leu	Glu	Ala	Ala	Leu	Val	Leu	Met	Glu	Ala	Ala	Pro	Glu	Leu	
				95					100					105	
Val	Phe	Glu	Pro	Thr	Thr	Cys	Glu	Ala	Phe	Ala	Gly	Gln	Thr	Ala	
				110					115					120	
Leu	His	Ile	Ala	Val	Val	Asn	Gln	Asn	Val	Asn	Leu	Val	Arg	Ala	
				125					130					135	
Leu	Leu	Thr	Arg	Arg	Ala	Ser	Val	Ser	Ala	Arg	Ala	Thr	Gly	Thr	
				140					145					150	
Ala	Phe	Arg	Arg	Ser	Pro	Arg	Asn	Leu	Ile	Tyr	Phe	Gly	Glu	His	
				155					160					165	
Pro	Leu	Ser	Phe	Ala	Ala	Cys	Val	Asn	Ser	Glu	Glu	Ile	Val	Arg	
				170					175					180	
Leu	Leu	Ile	Glu	His	Gly	Ala	Asp	Ile	Arg	Ala	Gln	Asp	Ser	Leu	
				185					190					195	
Gly	Asn	Thr	Val	Leu	His	Ile	Leu	Ile	Leu	Gln	Pro	Asn	Lys	Thr	
				200					205					210	
Phe	Ala	Cys	Gln	Met	Tyr	Asn	Leu	Leu	Leu	Ser	Tyr	Asp	Gly	His	
				215					220					225	
Gly	Asp	His	Leu	Gln	Pro	Leu	Asp	Leu	Val	Pro	Asn	His	Gln	Gly	
				230					235					240	
Leu	Thr	Pro	Phe	Lys	Leu	Ala	Gly	Val	Glu	Gly	Asn	Thr	Val	Met	
				245					250					255	
Phe	Gln	His	Leu	Met	Gln	Lys	Arg	Arg	His	Ile	Gln	Trp	Thr	Tyr	
				260					265					270	
Gly	Pro	Leu	Thr	Ser	Ile	Leu	Tyr	Asp	Leu	Thr	Glu	Ile	Asp	Ser	
				275					280					285	
Trp	Gly	Glu	Glu	Leu	Ser	Phe	Leu	Glu	Leu	Val	Val	Ser	Ser	Asp	
				290					295					300	
Lys	Arg	Glu	Ala	Arg	Gln	Ile	Leu	Glu	Gln	Thr	Pro	Val	Lys	Glu	
				305					310					315	
Leu	Val	Ser	Phe	Lys	Trp	Asn	Lys	Tyr	Gly	Arg	Pro	Tyr	Phe	Cys	
				320					325					330	
Ile	Leu	Ala	Ala	Leu	Tyr	Leu	Leu	Tyr	Met	Ile	Cys	Phe	Thr	Thr	
				335					340					345	
Cys	Cys	Val	Tyr	Arg	Pro	Leu	Lys	Phe	Arg	Gly	Gly	Asn	Arg	Thr	
				350					355					360	
His	Ser	Arg	Asp	Ile	Thr	Ile	Leu	Gln	Gln	Lys	Leu	Leu	Gln	Glu	
				365					370					375	
Ala	Tyr	Glu	Thr	Arg	Glu	Asp	Ile	Ile	Arg	Leu	Val	Gly	Glu	Leu	
				380					385					390	
Val	Ser	Ile	Val	Gly	Ala	Val	Ile	Ile	Leu	Leu	Leu	Glu	Ile	Pro	
				395					400					405	
Asp	Ile	Phe	Arg	Val	Gly	Ala	Ser	Arg	Tyr	Phe	Gly	Lys	Thr	Ile	
				410					415					420	
Leu	Gly	Gly	Pro	Phe	His	Val	Ile	Met	Ile	Thr	Tyr	Ala	Ser	Leu	
				425					430					435	
Val	Leu	Val	Thr	Met	Val	Met	Arg	Leu	Thr	Asn	Thr	Asn	Gly	Glu	
				440					445					450	
Val	Val	Pro	Met	Ser	Phe	Ala	Leu	Val	Leu	Gly	Trp	Cys	Ser	Val	
				455					460					465	
Met	Tyr	Phe	Thr	Arg	Gly	Phe	Gln	Met	Leu	Gly	Pro	Phe	Thr	Ile	
				470					475					480	

Met	Ile	Gln	Lys	Met	Ile	Phe	Gly	Asp	Leu	Met	Arg	Phe	Cys	Trp	
				485					490					495	
Leu	Met	Ala	Val	Val	Ile	Leu	Gly	Phe	Ala	Ser	Ala	Phe	Tyr	Ile	
				500					505					510	
Ile	Phe	Gln	Thr	Glu	Asp	Pro	Thr	Ser	Leu	Gly	Gln	Phe	Tyr	Asp	
				515					520					525	
Tyr	Pro	Met	Ala	Leu	Phe	Thr	Thr	Phe	Glu	Leu	Phe	Leu	Thr	Val	
				530					535					540	
Ile	Asp	Ala	Pro	Ala	Asn	Tyr	Asp	Val	Asp	Leu	Pro	Phe	Met	Phe	
				545					550					555	
Ser	Ile	Val	Asn	Phe	Ala	Phe	Ala	Ile	Ile	Ala	Thr	Leu	Leu	Met	
				560					565					570	
Leu	Asn	Leu	Phe	Ile	Ala	Met	Met	Gly	Asp	Thr	His	Trp	Arg	Val	
				575					580					585	
Ala	Gln	Glu	Arg	Asp	Glu	Leu	Trp	Arg	Ala	Gln	Val	Val	Ala	Thr	
				590					595					600	
Thr	Val	Met	Leu	Glu	Arg	Lys	Leu	Pro	Arg	Cys	Leu	Trp	Pro	Arg	
				605					610					615	
Ser	Gly	Ile	Cys	Gly	Cys	Glu	Phe	Gly	Leu	Gly	Asp	Arg	Trp	Phe	
				620					625					630	
Leu	Arg	Val	Glu	Asn	His	Asn	Asp	Gln	Asn	Pro	Leu	Arg	Val	Leu	
				635					640					645	
Arg	Tyr	Val	Glu	Val	Phe	Lys	Asn	Ser	Asp	Lys	Glu	Asp	Asp	Gln	
				650					655					660	
Glu	His	Pro	Ser	Glu	Lys	Gln	Pro	Ser	Gly	Ala	Glu	Ser	Gly	Thr	
				665					670					675	
Leu	Ala	Arg	Ala	Ser	Leu	Ala	Leu	Pro	Thr	Ser	Ser	Leu	Ser	Arg	
				680					685					690	
Thr	Ala	Ser	Gln	Ser	Ser	Ser	His	Arg	Gly	Trp	Glu	Ile	Leu	Arg	
				695					700					705	
Gln	Asn	Thr	Leu	Gly	His	Leu	Asn	Leu	Gly	Leu	Asn	Leu	Ser	Glu	
				710					715					720	
Gly	Asp	Gly	Glu	Glu	Val	Tyr	His	Phe							
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<211> 492

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1471717CD1

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Lys	Leu	Ser	Leu	Gly	Thr	Ala	Glu	Pro	Gln	Val	Lys	Glu	Pro	Lys	
				20					25					30	
Thr	Phe	Thr	Val	Glu	Asp	Ala	Val	Glu	Thr	Ile	Gly	Phe	Gly	Arg	
				35					40					45	
Phe	His	Ile	Ala	Leu	Phe	Leu	Ile	Met	Gly	Ser	Thr	Gly	Val	Val	
				50					55					60	
Glu	Ala	Met	Glu	Ile	Met	Leu	Ile	Ala	Val	Val	Ser	Pro	Val	Ile	
				65					70					75	
Arg	Cys	Glu	Trp	Gln	Leu	Glu	Asn	Trp	Gln	Val	Ala	Leu	Val	Thr	
				80					85					90	
Thr	Met	Val	Phe	Phe	Gly	Tyr	Met	Val	Phe	Ser	Ile	Leu	Phe	Gly	
				95					100					105	
Leu	Leu	Ala	Asp	Arg	Tyr	Gly	Arg	Trp	Lys	Ile	Leu	Leu	Ile	Ser	
				110					115					120	
Phe	Leu	Trp	Gly	Ala	Tyr	Phe	Ser	Leu	Leu	Thr	Ser	Phe	Ala	Pro	
				125					130					135	
Ser	Tyr	Ile	Trp	Phe	Val	Phe	Leu	Arg	Thr	Met	Val	Gly	Cys	Gly	
				140					145					150	
Val	Ser	Gly	His	Ser	Gln	Gly	Leu	Ile	Ile	Lys	Thr	Glu	Phe	Leu	
				155					160					165	

Pro	Thr	Lys	Tyr	Arg	Gly	Tyr	Met	Leu	Pro	Leu	Ser	Gln	Val	Phe	
				170					175					180	
Trp	Leu	Ala	Gly	Ser	Leu	Leu	Ile	Ile	Gly	Leu	Ala	Ser	Val	Ile	
				185					190					195	
Ile	Pro	Thr	Ile	Gly	Trp	Arg	Trp	Leu	Ile	Arg	Val	Ala	Ser	Ile	
				200					205					210	
Pro	Gly	Ile	Ile	Leu	Ile	Val	Ala	Phe	Lys	Phe	Ile	Pro	Glu	Ser	
				215					220					225	
Ala	Arg	Phe	Asn	Val	Ser	Thr	Gly	Asn	Thr	Arg	Ala	Ala	Leu	Ala	
				230					235					240	
Thr	Leu	Glu	Arg	Val	Ala	Lys	Met	Asn	Arg	Ser	Val	Met	Pro	Glu	
				245					250					255	
Gly	Lys	Leu	Val	Glu	Pro	Val	Leu	Glu	Lys	Arg	Gly	Arg	Phe	Ala	
				260					265					270	
Asp	Leu	Leu	Asp	Ala	Lys	Tyr	Leu	Arg	Thr	Thr	Leu	Gln	Ile	Trp	
				275					280					285	
Val	Ile	Trp	Leu	Gly	Ile	Ser	Phe	Ala	Tyr	Tyr	Gly	Val	Ile	Leu	
				290					295					300	
Ala	Ser	Ala	Glu	Leu	Leu	Glu	Arg	Asp	Leu	Val	Cys	Gly	Ser	Lys	
				305					310					315	
Ser	Asp	Ser	Ala	Val	Val	Val	Thr	Gly	Gly	Asp	Ser	Gly	Glu	Ser	
				320					325					330	
Gln	Ser	Pro	Cys	Tyr	Cys	His	Met	Phe	Ala	Pro	Ser	Asp	Tyr	Arg	
				335					340					345	
Thr	Met	Ile	Ile	Ser	Thr	Ile	Gly	Glu	Ile	Ala	Leu	Asn	Pro	Leu	
				350					355					360	
Asn	Ile	Leu	Gly	Ile	Asn	Phe	Leu	Gly	Arg	Arg	Leu	Ser	Leu	Ser	
				365					370					375	
Ile	Thr	Met	Gly	Cys	Thr	Ala	Leu	Phe	Cys	Leu	Leu	Leu	Asn	Ile	
				380					385					390	
Cys	Thr	Ser	Ser	Ala	Gly	Leu	Ile	Gly	Phe	Leu	Phe	Met	Leu	Arg	
				395					400					405	
Ala	Leu	Val	Ala	Ala	Asn	Phe	Asn	Thr	Val	Tyr	Ile	Tyr	Thr	Ala	
				410					415					420	
Glu	Val	Tyr	Pro	Thr	Thr	Met	Arg	Ala	Leu	Gly	Met	Gly	Thr	Ser	
				425					430					435	
Gly	Ser	Leu	Cys	Arg	Ile	Gly	Ala	Met	Val	Ala	Pro	Phe	Ile	Ser	
				440					445					450	
Gln	Val	Leu	Met	Ser	Ala	Ser	Ile	Leu	Gly	Ala	Leu	Cys	Leu	Phe	
				455					460					465	
Ser	Ser	Val	Cys	Val	Val	Cys	Ala	Ile	Ser	Ala	Phe	Thr	Leu	Pro	
				470					475					480	
Ile	Glu	Thr	Lys	Gly	Arg	Ala	Leu	Gln	Gln	Ile	Lys				
				485					490						

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<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3874406CD1

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Leu	Cys	Lys	Asn	Phe	Leu	Lys	Lys	Trp	Arg	Met	Lys	Arg	Glu	Ser	
				20					25					30	
Leu	Leu	Glu	Trp	Gly	Leu	Ser	Ile	Leu	Leu	Gly	Leu	Cys	Ile	Ala	
				35					40					45	
Leu	Phe	Ser	Ser	Ser	Met	Arg	Asn	Val	Gln	Phe	Pro	Gly	Met	Ala	
				50					55					60	
Pro	Gln	Asn	Leu	Gly	Arg	Val	Asp	Lys	Phe	Asn	Ser	Ser	Ser	Leu	
				65					70					75	
Met	Val	Val	Tyr	Thr	Pro	Ile	Ser	Asn	Leu	Thr	Gln	Gln	Ile	Met	
				80					85					90	

Asn	Lys	Thr	Ala	Leu	Ala	Pro	Leu	Leu	Lys	Gly	Thr	Ser	Val	Ile
				95					100					105
Gly	Ala	Pro	Asn	Lys	Thr	His	Met	Asp	Glu	Ile	Leu	Leu	Glu	Asn
				110					115					120
Leu	Pro	Tyr	Ala	Met	Gly	Ile	Ile	Phe	Asn	Glu	Thr	Phe	Ser	Tyr
				125					130					135
Lys	Leu	Ile	Phe	Phe	Gln	Gly	Tyr	Asn	Ser	Pro	Leu	Trp	Lys	Glu
				140					145					150
Asp	Phe	Ser	Ala	His	Cys	Trp	Asp	Gly	Tyr	Gly	Glu	Phe	Ser	Cys
				155					160					165
Thr	Leu	Thr	Lys	Tyr	Trp	Asn	Arg	Gly	Phe	Val	Ala	Leu	Gln	Thr
				170					175					180
Ala	Ile	Asn	Thr	Ala	Ile	Ile	Glu	Val	Ala	Leu	Val	Phe	Leu	Met
				185					190					195
Ser	Val	Leu	Leu	Lys	Lys	Ala	Val	Leu	Thr	Asn	Leu	Val	Val	Phe
				200					205					210
Leu	Leu	Thr	Leu	Phe	Trp	Gly	Cys	Leu	Gly	Phe	Thr	Val	Phe	Tyr
				215					220					225
Glu	Gln	Leu	Pro	Ser	Ser	Leu	Glu	Trp	Ile	Leu	Asn	Ile	Cys	Ser
				230					235					240
Pro	Phe	Ala	Phe	Thr	Gly	Met	Ile		Gln	Ile	Ile	Lys	Leu	Asp
				245					250					255
Tyr	Asn	Leu	Asn	Gly	Val	Ile	Phe	Pro	Asp	Pro	Ser	Gly	Asp	Ser
				260					265					270
Tyr	Thr	Met	Ile	Ala	Thr	Phe	Ser	Met	Leu	Leu	Leu	Asp	Gly	Leu
				275					280					285
Ile	Tyr	Leu	Leu	Leu	Ala	Leu	Tyr	Phe	Asp	Lys	Ile	Leu	Pro	Tyr
				290					295					300
Gly	Asp	Glu	Arg	His	Tyr	Ser	Pro	Leu	Phe	Phe	Leu	Asn	Ser	Ser
				305					310					315
Ser	Cys	Phe	Gln	His	Gln	Arg	Thr	Asn	Ala	Lys	Val	Ile	Glu	Lys
				320					325					330
Glu	Ile	Asp	Ala	Glu	His	Pro	Ser	Asp	Asp	Tyr	Phe	Glu	Pro	Val
				335					340					345
Ala	Pro	Glu	Phe	Gln	Gly	Lys	Glu	Ala	Ile	Arg	Ile	Arg	Asn	Val
				350					355					360
Lys	Lys	Glu	Tyr	Lys	Gly	Lys	Ser	Gly	Lys	Val	Glu	Ala	Leu	Lys
				365					370					375
Gly	Leu	Leu	Phe	Asp	Ile	Tyr	Glu	Gly	Gln	Ile	Thr	Ala	Ile	Leu
				380					385					390
Gly	His	Ser	Gly	Ala	Gly	Lys	Ser	Ser	Leu	Leu	Asn	Ile	Leu	Asn
				395					400					405
Gly	Leu	Ser	Val	Pro	Thr	Glu	Gly	Ser	Val	Thr	Ile	Tyr	Asn	Lys
				410					415					420
Asn	Leu	Ser	Glu	Met	Gln	Asp	Leu	Glu	Glu	Ile	Arg	Lys	Ile	Thr
				425					430					435
Gly	Val	Cys	Pro	Gln	Phe	Asn	Val	Gln	Phe	Asp	Ile	Leu	Thr	Val
				440					445					450
Lys	Glu	Asn	Leu	Ser	Leu	Phe	Ala	Lys	Ile	Lys	Gly	Ile	His	Leu
				455					460					465
Lys	Glu	Val	Glu	Gln	Glu	Val	Gln	Arg	Ile	Leu	Leu	Glu	Leu	Asp
				470					475					480
Met	Gln	Asn	Ile	Gln	Asp	Asn	Leu	Ala	Lys	His	Leu	Ser	Glu	Gly
				485					490					495
Gln	Lys	Arg	Lys	Leu	Thr	Phe	Gly	Ile	Thr	Ile	Leu	Gly	Asp	Pro
				500					505					510
Gln	Ile	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Thr	Gly	Leu	Asp	Pro	Phe
				515					520					525
Ser	Arg	Asp	Gln	Val	Trp	Ser	Leu	Leu	Arg	Glu	Arg	Arg	Ala	Asp
				530					535					540
His	Val	Ile	Leu	Phe	Ser	Thr	Gln	Ser	Met	Asp	Glu	Ala	Asp	Ile
				545					550					555
Leu	Ala	Asp	Arg	Lys	Val	Ile	Met	Ser	Asn	Gly	Arg	Leu	Lys	Cys
				560					565					570
Ala	Gly	Ser	Ser	Ile	Phe	Leu	Lys	Arg	Arg	Trp	Gly	Leu	Gly	Tyr
				575					580					585
His	Leu	Ser	Leu	His	Arg	Asn	Glu	Ile	Cys	Asn	Pro	Glu	Gln	Ile

Thr Ser Phe Ile	590	Thr His His Ile Pro	595	Asp Ala Lys Leu Lys	600
Glu Asn Lys Glu	605	Lys Leu Val Tyr Thr	610	Leu Pro Leu Glu Arg	615
Asn Thr Phe Pro	620	Asp Leu Phe Ser Asp	625	Leu Asp Lys Cys Ser	630
Gln Gly Val Thr	635	Gly Tyr Asp Ile Ser	640	Met Ser Thr Leu Asn	645
Val Phe Met Lys	650	Leu Glu Gly Gln Ser	655	Thr Ile Glu Gln Asp	660
Glu Gln Val Glu	665	Met Ile Arg Asp Ser	670	Glu Ser Leu Asn Glu	675
Glu Leu Ala His	680	Ser Ser Phe Ser Glu	685	Met Gln Thr Ala Val	690
Asp Met Gly Leu	695	Trp Arg Met Gln Val	700	Phe Ala Met Ala Arg	705
Arg Phe Leu Lys	710	Leu Lys Arg Gln Thr	715	Lys Val Leu Leu Thr	720
Leu Leu Val Phe	725	Gly Ile Ala Ile Phe	730	Pro Leu Ile Val Glu	735
Ile Ile Tyr Ala	740	Met Leu Asn Glu Lys	745	Ile Asp Trp Glu Phe	750
Asn Glu Leu Tyr	755	Phe Leu Ser Pro Gly	760	Gln Leu Pro Gln Glu	765
Arg Thr Ser Leu	770	Leu Ile Ile Asn Asn	775	Thr Glu Ser Asn Ile	780
Asp Phe Ile Lys	785	Ser Leu Lys His Gln	790	Asn Ile Leu Leu Glu	795
Asp Asp Phe Glu	800	Asn Arg Asn Gly Thr	805	Asp Gly Leu Ser Tyr	810
Gly Ala Ile Ile	815	Val Ser Gly Lys Gln	820	Lys Asp Tyr Arg Phe	825
Val Val Cys Asn	830	Thr Lys Arg Leu His	835	Cys Phe Pro Ile Leu	840
Asn Ile Ile Ser	845	Asn Gly Leu Leu Gln	850	Met Phe Asn His Thr	855
His Ile Arg Ile	860	Glu Ser Ser Pro Phe	865	Pro Leu Ser His Ile	870
Leu Trp Thr Gly	875	Leu Pro Asp Gly Ser	880	Phe Phe Leu Phe Leu	885
Leu Cys Ser Ile	890	Ser Pro Tyr Ile Thr	895	Met Gly Ser Ile Ser	900
Tyr Lys Lys Asn	905	Ala Lys Ser Gln Leu	910	Trp Ile Ser Gly Leu	915
Thr Ser Ala Tyr	920	Trp Cys Gly Gln Ala	925	Leu Val Asp Val Ser	930
Phe Ile Leu Ile	935	Leu Leu Leu Met Tyr	940	Leu Ile Phe Tyr Ile	945
Asn Met Gln Tyr	950	Leu Leu Ile Thr Ser	955	Gln Ile Val Phe Ala	960
Val Ile Val Thr	965	Pro Gly Tyr Ala Ala	970	Ser Leu Val Phe Phe	975
Tyr Met Ile Ser	980	Phe Ile Phe Arg Lys	985	Arg Arg Lys Asn Ser	990
Leu Trp Ser Phe	995	Tyr Phe Phe Phe Ala	1000	Thr Ile Met Phe Ser	1005
Ile Thr Leu Ile	1010	Asn His Phe Asp Leu	1015	Ser Ile Leu Ile Thr	1020
Met Val Leu Val	1025	Pro Ser Tyr Thr Leu	1030	Leu Gly Phe Lys Thr	1035
Leu Glu Val Arg	1040	Asp Gln Glu His Tyr	1045	Arg Glu Phe Pro Glu	1050
Asn Phe Glu Leu	1055	Ser Ala Thr Asp Phe	1060	Leu Val Cys Phe Ile	1065
Tyr Phe Gln Thr	1070	Leu Leu Phe Val Phe	1075	Val Leu Arg Cys Met	1080
	1085		1090		1095

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Leu Lys Cys Gly Lys Lys Arg Met Arg Lys Asp Pro Val Phe Arg
1100 1105 1110
Ile Ser Pro Gln Ser Arg Asp Ala Lys Pro Asn Pro Glu Glu Pro
1115 1120 1125
Ile Asp Glu Asp Glu Asp Ile Gln Thr Glu Arg Ile Arg Thr Val
1130 1135 1140
Thr Ala Leu Thr Thr Ser Ile Leu Asp Glu Lys Pro Val Ile Ile
1145 1150 1155
Ala Ser Cys Leu His Lys Glu Tyr Ala Gly Gln Lys Lys Ser Cys
1160 1165 1170
Phe Ser Lys Arg Lys Lys Lys Ile Ala Ala Arg Asn Ile Ser Phe
1175 1180 1185
Cys Val Gln Glu Gly Glu Ile Leu Gly Leu Leu Gly Pro Ser Gly
1190 1195 1200
Ala Gly Lys Ser Ser Ser Ile Arg Met Ile Ser Gly Ile Thr Lys
1205 1210 1215
Pro Thr Ala Gly Glu Val Glu Leu Lys Gly Cys Ser Ser Val Leu
1220 1225 1230
Gly His Leu Gly Tyr Cys Pro Gln Glu Asn Val Leu Trp Pro Met
1235 1240 1245
Leu Thr Leu Arg Glu His Leu Glu Val Tyr Ala Ala Val Lys Gly
1250 1255 1260
Leu Arg Glu Ala Asp Ala Arg Leu Ala Ile Ala Arg Leu Val Ser
1265 1270 1275
Ala Phe Lys Leu His Glu Gln Leu Asn Val Pro Val Gln Lys Leu
1280 1285 1290
Thr Ala Gly Ile Thr Arg Lys Leu Cys Phe Val Leu Ser Leu Leu
1295 1300 1305
Gly Asn Ser Pro Val Leu Leu Leu Asp Glu Pro Ser Thr Gly Ile
1310 1315 1320
Asp Pro Thr Gly Gln Gln Gln Met Trp Gln Ala Ile Gln Ala Val
1325 1330 1335
Val Lys Asn Thr Glu Arg Gly Val Leu Leu Thr Thr His Asn Leu
1340 1345 1350
Ala Glu Ala Glu Ala Leu Cys Asp Arg Val Ala Ile Met Val Ser
1355 1360 1365
Gly Arg Leu Arg Cys Ile Gly Ser Ile Gln His Leu Lys Asn Lys
1370 1375 1380
Leu Gly Lys Asp Tyr Ile Leu Glu Leu Lys Val Lys Glu Thr Ser
1385 1390 1395
Gln Val Thr Leu Val His Thr Glu Ile Leu Lys Leu Phe Pro Gln
1400 1405 1410
Ala Ala Gly Gln Gln Arg Tyr Ser Ser Leu Leu Thr Tyr Lys Leu
1415 1420 1425
Pro Val Ala Asp Val Tyr Pro Leu Ser Gln Thr Phe His Lys Leu
1430 1435 1440
Glu Ala Val Lys His Asn Phe Asn Leu Glu Glu Tyr Ser Leu Ser
1445 1450 1455
Gln Cys Thr Leu Glu Lys Val Phe Leu Glu Leu Ser Lys Glu Gln
1460 1465 1470
Glu Val Gly Asn Phe Asp Glu Glu Ile Asp Thr Thr Met Arg Trp
1475 1480 1485
Lys Leu Leu Pro His Ser Asp Glu Pro
1490

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Thr	Pro	Gly	Leu	Glu	Ala	Val	Pro	Pro	Val	Ala	Pro	Pro	Pro	Ala	30
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Thr	Ala	Ala	Ser	Gly	Pro	Ile	Pro	Lys	Ser	Gly	Pro	Glu	Pro	Lys	35
				35					40						45
Arg	Arg	His	Leu	Gly	Thr	Leu	Leu	Gln	Pro	Thr	Val	Asn	Lys	Phe	50
				50					55						60
Ser	Leu	Arg	Val	Phe	Gly	Ser	His	Lys	Ala	Val	Glu	Ile	Glu	Gln	65
				65					70						75
Glu	Arg	Val	Lys	Ser	Ala	Gly	Ala	Trp	Ile	Ile	His	Pro	Tyr	Ser	80
				80					85						90
Asp	Phe	Arg	Phe	Tyr	Trp	Asp	Leu	Ile	Met	Leu	Leu	Leu	Met	Val	95
				95					100						105
Gly	Asn	Leu	Ile	Val	Leu	Pro	Val	Gly	Ile	Thr	Phe	Phe	Lys	Glu	110
				110					115						120
Glu	Asn	Ser	Pro	Pro	Trp	Ile	Val	Phe	Asn	Val	Leu	Ser	Asp	Thr	125
				125					130						135
Phe	Phe	Leu	Leu	Asp	Leu	Val	Leu	Asn	Phe	Arg	Thr	Gly	Ile	Val	140
				140					145						150
Val	Glu	Glu	Gly	Ala	Glu	Ile	Leu	Leu	Ala	Pro	Arg	Ala	Ile	Arg	155
				155					160						165
Thr	Arg	Tyr	Leu	Arg	Thr	Trp	Phe	Leu	Val	Asp	Leu	Ile	Ser	Ser	170
				170					175						180
Ile	Pro	Val	Asp	Tyr	Ile	Phe	Leu	Val	Val	Glu	Leu	Glu	Pro	Arg	185
				185					190						195
Leu	Asp	Ala	Glu	Val	Tyr	Lys	Thr	Ala	Arg	Ala	Leu	Arg	Ile	Val	200
				200					205						210
Arg	Phe	Thr	Lys	Ile	Leu	Ser	Leu	Leu	Arg	Leu	Leu	Arg	Leu	Ser	215
				215					220						225
Arg	Leu	Ile	Arg	Tyr	Ile	His	Gln	Trp	Glu	Glu	Ile	Phe	His	Met	230
				230					235						240
Thr	Tyr	Asp	Leu	Ala	Ser	Ala	Val	Val	Arg	Ile	Phe	Asn	Leu	Ile	245
				245					250						255
Gly	Met	Met	Leu	Leu	Leu	Cys	His	Trp	Asp	Gly	Cys	Leu	Gln	Phe	260
				260					265						270
Leu	Val	Pro	Met	Leu	Gln	Asp	Phe	Pro	Pro	Asp	Cys	Trp	Val	Ser	275
				275					280						285
Ile	Asn	His	Met	Val	Asn	His	Ser	Trp	Gly	Arg	Gln	Tyr	Ser	His	290
				290					295						300
Ala	Leu	Phe	Lys	Ala	Met	Ser	His	Met	Leu	Cys	Ile	Gly	Tyr	Gly	305
				305					310						315
Gln	Gln	Ala	Pro	Val	Gly	Met	Pro	Asp	Val	Trp	Leu	Thr	Met	Leu	320
				320					325						330
Ser	Met	Ile	Val	Gly	Ala	Thr	Cys	Tyr	Ala	Met	Phe	Ile	Gly	His	335
				335					340						345
Ala	Thr	Ala	Leu	Ile	Gln	Ser	Leu	Asp	Ser	Ser	Arg	Arg	Gln	Tyr	350
				350					355						360
Gln	Glu	Lys	Tyr	Lys	Gln	Val	Glu	Gln	Tyr	Met	Ser	Phe	His	Lys	365
				365					370						375
Leu	Pro	Ala	Asp	Thr	Arg	Gln	Arg	Ile	His	Glu	Tyr	Tyr	Glu	His	380
				380					385						390
Arg	Tyr	Gln	Gly	Lys	Met	Phe	Asp	Glu	Glu	Ser	Ile	Leu	Gly	Glu	395
				395					400						405
Leu	Ser	Glu	Pro	Leu	Arg	Glu	Glu	Ile	Ile	Asn	Phe	Thr	Cys	Arg	410
				410					415						420
Gly	Leu	Val	Ala	His	Met	Pro	Leu	Phe	Ala	His	Ala	Asp	Pro	Ser	425
				425					430						435
Phe	Val	Thr	Ala	Val	Leu	Thr	Lys	Leu	Arg	Phe	Glu	Val	Phe	Gln	440
				440					445						450
Pro	Gly	Asp	Leu	Val	Val	Arg	Glu	Gly	Ser	Val	Gly	Arg	Lys	Met	455
				455					460						465
Tyr	Phe	Ile	Gln	His	Gly	Leu	Leu	Ser	Val	Leu	Ala	Arg	Gly	Ala	470
				470					475						480
Arg	Asp	Thr	Arg	Leu	Thr	Asp	Gly	Ser	Tyr	Phe	Gly	Glu	Ile	Cys	485
				485					490						495
Leu	Leu	Thr	Arg	Gly	Arg	Arg	Thr	Ala	Ser	Val	Arg	Ala	Asp	Thr	500
				500					505						510
Tyr	Cys	Arg	Leu	Tyr	Ser	Leu	Ser	Val	Asp	His	Phe	Asn	Ala	Val	

Leu Glu Glu Phe	515	Pro Met Met Arg Arg	520	Ala Phe Glu Thr Val	525
Met Asp Arg Leu	530	Leu Arg Ile Gly Lys	535	Lys Asn Ser Ile Leu	540
Arg Lys Arg Ser	545	Glu Pro Ser Pro Gly	550	Ser Ser Gly Gly Ile	555
Glu Gln His Leu	560	Val Gln His Asp Arg	565	Asp Met Ala Arg Gly	570
Arg Gly Arg Ala	575	Pro Ser Thr Gly Ala	580	Gln Leu Ser Gly Lys	585
Val Leu Trp Glu	590	Pro Leu Val His Ala	595	Pro Leu Gln Ala Ala	600
Val Thr Ser Asn	605	Val Ala Ile Ala Leu	610	Thr His Gln Arg Gly	615
Leu Pro Leu Ser	620	Pro Asp Ser Pro Ala	625	Thr Leu Leu Ala Arg	630
Ala Trp Arg Ser	635	Ala Gly Ser Pro Ala	640	Ser Pro Leu Val Pro	645
Arg Ala Gly Pro	650	Trp Ala Ser Thr Ser	655	Arg Leu Pro Ala Pro	660
Ala Arg Thr Leu	665	His Ala Ser Leu Ser	670	Arg Ala Gly Arg Ser	675
Val Ser Leu Leu	680	Gly Pro Pro Pro Gly	685	Gly Gly Gly Arg Arg	690
Gly Pro Arg Gly	695	Arg Pro Leu Ser Ala	700	Ser Gln Pro Ser Leu	705
Gln Arg Ala Thr	710	Gly Asp Gly Ser Pro	715	Gly Arg Lys Gly Ser	720
Ser Glu Arg Leu	725	Pro Pro Ser Gly Leu	730	Leu Ala Lys Pro Pro	735
Thr Ala Gln Pro	740	Pro Arg Pro Pro Val	745	Pro Glu Pro Ala Thr	750
Arg Gly Leu Gln	755	Leu Ser Ala Asn Met	760		765
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<211> 614

<212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 5047435CD1

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	20	25
Gln Gly Arg Arg	Asp Arg Gly Gly Gly	Gly Pro Glu Ser Leu Ser
	35	40
Gly Gly Ser Gly	Val Gly Asp Ser Gly	Gly Gly Cys Ala Pro Gly
	50	55
Pro Ser Ala Pro	Pro Ala Arg Arg Arg	Val Pro Leu Ala Met Gly
	65	70
His Ser Pro Pro	Val Leu Pro Leu Cys	Ala Ser Val Ser Leu Leu
	80	85
Gly Gly Leu Thr	Phe Gly Tyr Glu Leu	Ala Val Ile Ser Gly Ala
	95	100
Leu Leu Pro Leu	Gln Leu Asp Phe Gly	Leu Ser Cys Leu Glu Gln
	110	115
Glu Phe Leu Val	Gly Ser Leu Leu Leu	Gly Ala Leu Leu Ala Ser
	125	130
Leu Val Gly Gly	Phe Leu Ile Asp Cys	Tyr Gly Arg Lys Gln Ala
	140	145
Ile Leu Gly Ser	Asn Leu Val Leu Leu	Ala Gly Ser Leu Thr Leu

	155		160		165
Gly Leu Ala Gly	Ser Leu Ala Trp Leu	Val Leu Gly Arg Ala	Val		
	170		175		180
Val Gly Phe Ala	Ile Ser Leu Ser Ser	Met Ala Cys Cys Ile	Tyr		
	185		190		195
Val Ser Glu Leu	Val Gly Pro Arg Gln	Arg Gly Val Leu Val	Ser		
	200		205		210
Leu Tyr Glu Ala	Gly Ile Thr Val Gly	Ile Leu Leu Ser Tyr	Ala		
	215		220		225
Leu Asn Tyr Ala	Leu Ala Gly Thr Pro	Trp Gly Trp Arg His	Met		
	230		235		240
Phe Gly Trp Ala	Thr Ala Pro Ala Val	Leu Gln Ser Leu Ser	Leu		
	245		250		255
Leu Phe Leu Pro	Ala Gly Thr Asp Glu	Thr Ala Thr His Lys	Asp		
	260		265		270
Leu Ile Pro Leu	Gln Gly Gly Glu Ala	Pro Lys Leu Gly Pro	Gly		
	275		280		285
Arg Pro Arg Tyr	Ser Phe Leu Asp Leu	Phe Arg Ala Arg Asp	Asn		
	290		295		300
Met Arg Gly Arg	Thr Val Gly Leu Gly	Leu Val Leu Phe	Gln		
	305		310		315
Gln Leu Thr Gly	Gln Pro Asn Val Leu	Cys Tyr Ala Ser Thr	Ile		
	320		325		330
Phe Ser Ser Val	Gly Phe His Gly Gly	Ser Ser Ala Val Leu	Ala		
	335		340		345
Ser Val Gly Leu	Gly Ala Val Lys Val	Ala Ala Thr Leu Thr	Ala		
	350		355		360
Met Gly Leu Val	Asp Arg Ala Gly Arg	Arg Ala Leu Leu Leu	Ala		
	365		370		375
Gly Cys Ala Leu	Met Ala Leu Ser Val	Ser Gly Ile Gly Leu	Val		
	380		385		390
Ser Phe Ala Val	Pro Met Asp Ser Gly	Pro Ser Cys Leu Ala	Val		
	395		400		405
Pro Asn Ala Thr	Gly Gln Thr Gly Leu	Pro Gly Asp Ser Gly	Leu		
	410		415		420
Leu Gln Asp Ser	Ser Leu Pro Pro Ile	Pro Arg Thr Asn Glu	Asp		
	425		430		435
Gln Arg Glu Pro	Ile Leu Ser Thr Ala	Lys Lys Thr Lys Pro	His		
	440		445		450
Pro Arg Ser Gly	Asp Pro Ser Ala Pro	Pro Arg Leu Ala Leu	Ser		
	455		460		465
Ser Ala Leu Pro	Gly Pro Pro Leu Pro	Ala Arg Gly His Ala	Leu		
	470		475		480
Leu Arg Trp Thr	Ala Leu Leu Cys Leu	Met Val Phe Val Ser	Ala		
	485		490		495
Phe Ser Phe Gly	Phe Gly Pro Val Thr	Trp Leu Val Leu Ser	Glu		
	500		505		510
Ile Tyr Pro Val	Glu Ile Arg Gly Arg	Ala Phe Ala Phe Cys	Asn		
	515		520		525
Ser Phe Asn Trp	Ala Ala Asn Leu Phe	Ile Ser Leu Ser Phe	Leu		
	530		535		540
Asp Leu Ile Gly	Thr Ile Gly Leu Ser	Trp Thr Phe Leu Leu	Tyr		
	545		550		555
Gly Leu Thr Ala	Val Leu Gly Leu Gly	Phe Ile Tyr Leu Phe	Val		
	560		565		570
Pro Glu Thr Lys	Gly Gln Ser Leu Ala	Glu Ile Asp Gln Gln	Phe		
	575		580		585
Gln Lys Arg Arg	Phe Thr Leu Ser Phe	Gly His Arg Gln Asn	Ser		
	590		595		600
Thr Gly Ile Pro	Tyr Ser Arg Ile Glu	Ile Ser Ala Ala Ser			
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<211> 2180

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475603CD1

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Val	Phe	Ser	Pro	Thr	Val	Val	Leu	Thr	Ser	Leu	Ser	Arg	Pro	Leu
				20					25					30
Pro	Ser	Leu	Thr	Met	Ala	Phe	Trp	Thr	Gln	Leu	Met	Leu	Leu	Leu
				35					40					45
Trp	Lys	Asn	Phe	Met	Tyr	Arg	Arg	Arg	Gln	Pro	Val	Gln	Leu	Leu
				50					55					60
Val	Glu	Leu	Leu	Trp	Pro	Leu	Phe	Leu	Phe	Phe	Ile	Leu	Val	Ala
				65					70					75
Val	Arg	His	Ser	His	Pro	Pro	Leu	Glu	His	His	Glu	Cys	His	Phe
				80					85					90
Pro	Asn	Lys	Pro	Leu	Pro	Ser	Ala	Gly	Thr	Val	Pro	Trp	Leu	Gln
				95					100					105
Gly	Leu	Ile	Cys	Asn	Val	Asn	Asn	Thr	Cys	Phe	Pro	Gln	Leu	Thr
				110					115					120
Pro	Gly	Glu	Glu	Pro	Gly	Arg	Leu	Ser	Asn	Phe	Asn	Asp	Ser	Leu
				125					130					135
Val	Ser	Arg	Leu	Leu	Ala	Asp	Ala	Arg	Thr	Val	Leu	Gly	Gly	Ala
				140					145					150
Ser	Ala	His	Arg	Thr	Leu	Ala	Gly	Leu	Gly	Lys	Leu	Ile	Ala	Thr
				155					160					165
Leu	Arg	Ala	Ala	Arg	Ser	Thr	Ala	Gln	Pro	Gln	Pro	Thr	Lys	Gln
				170					175					180
Ser	Pro	Leu	Glu	Pro	Pro	Met	Leu	Asp	Val	Ala	Glu	Leu	Leu	Thr
				185					190					195
Ser	Leu	Leu	Arg	Thr	Glu	Ser	Leu	Gly	Leu	Ala	Leu	Gly	Gln	Ala
				200					205					210
Gln	Glu	Pro	Leu	His	Ser	Leu	Leu	Glu	Ala	Ala	Glu	Asp	Leu	Ala
				215					220					225
Gln	Glu	Leu	Leu	Ala	Leu	Arg	Ser	Leu	Val	Glu	Leu	Arg	Ala	Leu
				230					235					240
Leu	Gln	Arg	Pro	Arg	Gly	Thr	Ser	Gly	Pro	Leu	Glu	Leu	Leu	Ser
				245					250					255
Glu	Ala	Leu	Cys	Ser	Val	Arg	Gly	Pro	Ser	Ser	Thr	Val	Gly	Pro
				260					265					270
Ser	Leu	Asn	Trp	Tyr	Glu	Ala	Ser	Asp	Leu	Met	Glu	Leu	Val	Gly
				275					280					285
Gln	Glu	Pro	Glu	Ser	Ala	Leu	Pro	Asp	Ser	Ser	Leu	Ser	Pro	Ala
				290					295					300
Cys	Ser	Glu	Leu	Ile	Gly	Ala	Leu	Asp	Ser	His	Pro	Leu	Ser	Arg
				305					310					315
Leu	Leu	Trp	Arg	Arg	Leu	Lys	Pro	Leu	Ile	Leu	Gly	Lys	Leu	Leu
				320					325					330
Phe	Ala	Pro	Asp	Thr	Pro	Phe	Thr	Arg	Lys	Leu	Met	Ala	Gln	Val
				335					340					345
Asn	Arg	Thr	Phe	Glu	Glu	Leu	Thr	Leu	Leu	Arg	Asp	Val	Arg	Glu
				350					355					360
Val	Trp	Glu	Met	Leu	Gly	Pro	Arg	Ile	Phe	Thr	Phe	Met	Asn	Asp
				365					370					375
Ser	Ser	Asn	Val	Ala	Met	Leu	Gln	Arg	Leu	Leu	Gln	Met	Gln	Asp
				380					385					390
Glu	Gly	Arg	Arg	Gln	Pro	Arg	Pro	Gly	Gly	Arg	Asp	His	Met	Glu
				395					400					405
Ala	Leu	Arg	Ser	Phe	Leu	Asp	Pro	Gly	Ser	Gly	Gly	Tyr	Ser	Trp
				410					415					420
Gln	Asp	Ala	His	Ala	Asp	Val	Gly	His	Leu	Val	Gly	Thr	Leu	Gly
				425					430					435
Arg	Val	Thr	Glu	Cys	Leu	Ser	Leu	Asp	Lys	Leu	Glu	Ala	Ala	Pro
				440					445					450
Ser	Glu	Ala	Ala	Leu	Val	Ser	Arg	Ala	Leu	Gln	Leu	Leu	Ala	Glu
				455					460					465

His	Arg	Phe	Trp	Ala	Gly	Val	Val	Phe	Leu	Gly	Pro	Glu	Asp	Ser
				470					475					480
Ser	Asp	Pro	Thr	Glu	His	Pro	Thr	Pro	Asp	Leu	Gly	Pro	Gly	His
				485					490					495
Val	Arg	Ile	Lys	Ile	Arg	Met	Asp	Ile	Asp	Val	Val	Thr	Arg	Thr
				500					505					510
Asn	Lys	Ile	Arg	Asp	Arg	Phe	Trp	Asp	Pro	Gly	Pro	Ala	Ala	Asp
				515					520					525
Pro	Leu	Thr	Asp	Leu	Arg	Tyr	Val	Trp	Gly	Gly	Phe	Val	Tyr	Leu
				530					535					540
Gln	Asp	Leu	Val	Glu	Arg	Ala	Ala	Val	Arg	Val	Leu	Ser	Gly	Ala
				545					550					555
Asn	Pro	Arg	Ala	Gly	Leu	Tyr	Leu	Gln	Gln	Met	Pro	Tyr	Pro	Cys
				560					565					570
Tyr	Val	Asp	Asp	Val	Phe	Leu	Arg	Val	Leu	Ser	Arg	Ser	Leu	Pro
				575					580					585
Leu	Phe	Leu	Thr	Leu	Ala	Trp	Ile	Tyr	Ser	Val	Thr	Leu	Thr	Val
				590					595					600
Lys	Ala	Val	Val	Arg	Glu	Lys	Glu	Thr	Arg	Leu	Arg	Asp	Thr	Met
				605					610					615
Arg	Ala	Met	Gly	Leu	Ser	Arg	Ala	Val	Leu	Trp	Leu	Gly	Trp	Phe
				620					625					630
Leu	Ser	Cys	Leu	Gly	Pro	Phe	Leu	Leu	Ser	Ala	Ala	Leu	Leu	Val
				635					640					645
Leu	Val	Leu	Lys	Leu	Gly	Asp	Ile	Leu	Pro	Tyr	Ser	His	Pro	Gly
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Val	Val	Phe	Leu	Phe	Leu	Ala	Ala	Phe	Ala	Val	Ala	Thr	Val	Thr
				665					670					675
Gln	Ser	Phe	Leu	Leu	Ser	Ala	Phe	Phe	Ser	Arg	Ala	Asn	Leu	Ala
				680					685					690
Ala	Ala	Cys	Gly	Gly	Leu	Ala	Tyr	Phe	Ser	Leu	Tyr	Leu	Pro	Tyr
				695					700					705
Val	Leu	Cys	Val	Ala	Trp	Arg	Asp	Arg	Leu	Pro	Ala	Gly	Gly	Arg
				710					715					720
Val	Ala	Ala	Ser	Leu	Leu	Ser	Pro	Val	Ala	Phe	Gly	Phe	Gly	Cys
				725					730					735
Glu	Ser	Leu	Ala	Leu	Leu	Glu	Glu	Gln	Gly	Glu	Gly	Ala	Gln	Trp
				740					745					750
His	Asn	Val	Gly	Thr	Arg	Pro	Thr	Ala	Asp	Val	Phe	Ser	Leu	Ala
				755					760					765
Gln	Val	Ser	Gly	Leu	Leu	Leu	Leu	Asp	Ala	Ala	Leu	Tyr	Gly	Leu
				770					775					780
Ala	Thr	Trp	Tyr	Leu	Glu	Ala	Val	Cys	Pro	Gly	Gln	Tyr	Gly	Ile
				785					790					795
Pro	Glu	Pro	Trp	Asn	Phe	Pro	Phe	Arg	Arg	Ser	Tyr	Trp	Cys	Gly
				800					805					810
Pro	Arg	Pro	Pro	Lys	Ser	Pro	Ala	Pro	Cys	Pro	Thr	Pro	Leu	Asp
				815					820					825
Pro	Lys	Val	Leu	Val	Glu	Glu	Ala	Pro	Pro	Gly	Leu	Ser	Pro	Gly
				830					835					840
Val	Ser	Val	Arg	Ser	Leu	Glu	Lys	Arg	Phe	Pro	Gly	Ser	Pro	Gln
				845					850					855
Pro	Ala	Leu	Arg	Gly	Leu	Ser	Leu	Asp	Phe	Tyr	Gln	Gly	His	Ile
				860					865					870
Thr	Ala	Phe	Leu	Gly	His	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Thr	Leu
				875					880					885
Ser	Ile	Leu	Ser	Gly	Leu	Phe	Pro	Pro	Ser	Gly	Gly	Ser	Ala	Phe
				890					895					900
Ile	Leu	Gly	His	Asp	Val	Arg	Ser	Ser	Met	Ala	Ala	Ile	Arg	Pro
				905					910					915
His	Leu	Gly	Val	Cys	Pro	Gln	Tyr	Asn	Val	Leu	Phe	Asp	Met	Leu
				920					925					930
Thr	Val	Asp	Glu	His	Val	Trp	Phe	Tyr	Gly	Arg	Leu	Lys	Gly	Leu
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Ser	Ala	Ala	Val	Val	Gly	Pro	Glu	Gln	Asp	Arg	Leu	Leu	Gln	Asp
				950					955					960
Val	Gly	Leu	Val	Ser	Lys	Gln	Ser	Val	Gln	Thr	Arg	His	Leu	Ser

Gly Gly Met Gln Arg	Lys Leu Ser Val Ala	Ile Ala Phe Val Gly	965	970	975
Gly Ser Gln Val Val	Ile Leu Asp Glu Pro	Thr Ala Gly Val Asp	980	985	990
Pro Ala Ser Arg Arg	Gly Ile Trp Glu Leu	Leu Leu Lys Tyr Arg	995	1000	1005
Glu Gly Arg Thr Leu	Ile Leu Ser Thr His	His Leu Asp Glu Ala	1010	1015	1020
Glu Leu Leu Gly Asp	Arg Val Ala Val Val	Ala Gly Gly Arg Leu	1025	1030	1035
Cys Cys Cys Gly Ser	Pro Leu Phe Leu Arg	Arg His Leu Gly Ser	1040	1045	1050
Gly Tyr Tyr Leu Thr	Leu Val Lys Ala Arg	Leu Pro Leu Thr Thr	1055	1060	1065
Asn Glu Lys Ala Asp	Thr Asp Met Glu Gly	Ser Val Asp Thr Arg	1070	1075	1080
Gln Glu Lys Lys Asn	Gly Ser Gln Gly Ser	Arg Val Gly Thr Pro	1085	1090	1095
Gln Leu Leu Ala Leu	Val Gln His Trp Val	Pro Gly Ala Arg Leu	1100	1105	1110
Val Glu Glu Leu Pro	His Glu Leu Val Leu	Val Leu Pro Tyr Thr	1115	1120	1125
Gly Ala His Asp Gly	Ser Phe Ala Thr Leu	Phe Arg Glu Leu Asp	1130	1135	1140
Thr Arg Leu Ala Glu	Leu Arg Leu Thr Gly	Tyr Gly Ile Ser Asp	1145	1150	1155
Thr Ser Leu Glu Glu	Ile Phe Leu Lys Val	Val Glu Glu Cys Ala	1160	1165	1170
Ala Asp Thr Asp Met	Glu Asp Gly Ser Cys	Gly Gln His Leu Cys	1175	1180	1185
Thr Gly Ile Ala Gly	Leu Asp Val Thr Leu	Arg Leu Lys Met Pro	1190	1195	1200
Pro Gln Glu Thr Ala	Leu Glu Asn Gly Glu	Pro Ala Gly Ser Ala	1205	1210	1215
Pro Glu Thr Asp Gln	Gly Ser Gly Pro Asp	Ala Val Gly Arg Val	1220	1225	1230
Gln Gly Trp Ala Leu	Thr Arg Gln Gln Leu	Gln Ala Leu Leu Leu	1235	1240	1245
Lys Arg Phe Leu Leu	Ala Arg Arg Ser Arg	Arg Gly Leu Phe Ala	1250	1255	1260
Gln Ile Val Leu Pro	Ala Leu Phe Val Gly	Leu Ala Leu Val Phe	1265	1270	1275
Ser Leu Ile Val Pro	Pro Phe Gly His Tyr	Pro Ala Leu Arg Leu	1280	1285	1290
Ser Pro Thr Met Tyr	Gly Ala Gln Val Ser	Phe Phe Ser Glu Asp	1295	1300	1305
Ala Pro Gly Asp Pro	Gly Arg Ala Arg Leu	Leu Glu Ala Leu Leu	1310	1315	1320
Gln Glu Ala Gly Leu	Glu Glu Pro Pro Val	Gln His Ser Ser His	1325	1330	1335
Arg Phe Ser Ala Pro	Glu Val Pro Ala Glu	Val Ala Lys Val Leu	1340	1345	1350
Ala Ser Gly Asn Trp	Thr Pro Glu Ser Pro	Ser Pro Ala Cys Gln	1355	1360	1365
Cys Ser Arg Pro Gly	Ala Arg Arg Leu Leu	Pro Asp Cys Pro Ala	1370	1375	1380
Ala Ala Gly Gly Pro	Pro Pro Pro Gln Ala	Val Thr Gly Ser Gly	1385	1390	1395
Glu Val Val Gln Asn	Gln Thr Gly Arg Asn	Leu Ser Asp Phe Leu	1400	1405	1410
Val Lys Thr Tyr Pro	Arg Leu Val Arg Gln	Gly Leu Lys Thr Lys	1415	1420	1425
Lys Trp Val Asn Glu	Val Arg Tyr Gly Gly	Phe Ser Leu Gly Gly	1430	1435	1440
Arg Asp Pro Gly Leu	Pro Ser Gly Gln Glu	Leu Gly Arg Ser Val	1445	1450	1455
			1460	1465	1470

Glu	Glu	Leu	Trp	Ala	Leu	Leu	Ser	Pro	Leu	Pro	Gly	Gly	Ala	Leu
				1475					1480					1485
Asp	Arg	Val	Leu	Lys	Asn	Leu	Thr	Ala	Trp	Ala	His	Ser	Leu	Asp
				1490					1495					1500
Ala	Gln	Asp	Ser	Leu	Lys	Ile	Trp	Phe	Asn	Asn	Lys	Gly	Trp	His
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Ser	Met	Val	Ala	Phe	Val	Asn	Arg	Ala	Ser	Asn	Ala	Ile	Leu	Arg
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Ala	His	Leu	Pro	Pro	Gly	Pro	Ala	Arg	His	Ala	His	Ser	Ile	Thr
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Thr	Leu	Asn	His	Pro	Leu	Asn	Leu	Thr	Lys	Glu	Gln	Leu	Ser	Glu
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Ala	Ala	Leu	Met	Ala	Ser	Ser	Val	Asp	Val	Leu	Val	Ser	Ile	Cys
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Val	Val	Phe	Ala	Met	Ser	Phe	Val	Pro	Ala	Ser	Phe	Thr	Leu	Val
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Leu	Ile	Glu	Glu	Arg	Val	Thr	Arg	Ala	Lys	His	Leu	Gln	Leu	Met
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Gly	Gly	Leu	Ser	Pro	Thr	Leu	Tyr	Trp	Leu	Gly	Asn	Phe	Leu	Trp
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Asp	Met	Cys	Asn	Tyr	Leu	Val	Pro	Ala	Cys	Ile	Val	Val	Leu	Ile
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Phe	Leu	Ala	Phe	Gln	Gln	Arg	Ala	Tyr	Val	Ala	Pro	Ala	Asn	Leu
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Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Tyr	Gly	Trp	Ser	Ile	Thr	
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Pro	Leu	Met	Tyr	Pro	Ala	Ser	Phe	Phe	Phe	Ser	Val	Pro	Ser	Thr
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Ala	Tyr	Val	Val	Leu	Thr	Cys	Ile	Asn	Leu	Phe	Ile	Gly	Ile	Asn
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Gly	Ser	Met	Ala	Thr	Phe	Val	Leu	Glu	Leu	Phe	Ser	Asp	Gln	Lys
				1700					1705					1710
Leu	Gln	Glu	Val	Ser	Arg	Ile	Leu	Lys	Gln	Val	Phe	Leu	Ile	Phe
				1715					1720					1725
Pro	His	Phe	Cys	Leu	Gly	Arg	Gly	Leu	Ile	Asp	Met	Val	Arg	Asn
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Gln	Ala	Met	Ala	Asp	Ala	Phe	Glu	Arg	Leu	Gly	Asp	Arg	Gln	Phe
				1745					1750					1755
Gln	Ser	Pro	Leu	Arg	Trp	Glu	Val	Val	Gly	Lys	Asn	Leu	Leu	Ala
				1760					1765					1770
Met	Val	Ile	Gln	Gly	Pro	Leu	Phe	Leu	Leu	Phe	Thr	Leu	Leu	Leu
				1775					1780					1785
Gln	His	Arg	Ser	Gln	Leu	Leu	Pro	Gln	Pro	Arg	Val	Arg	Ser	Leu
				1790					1795					1800
Pro	Leu	Leu	Gly	Glu	Glu	Asp	Glu	Asp	Val	Ala	Arg	Glu	Arg	Glu
				1805					1810					1815
Arg	Val	Val	Gln	Gly	Ala	Thr	Gln	Gly	Asp	Val	Leu	Val	Leu	Arg
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Asn	Leu	Thr	Lys	Val	Tyr	Arg	Gly	Gln	Arg	Met	Pro	Ala	Val	Asp
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Arg	Leu	Cys	Leu	Gly	Ile	Pro	Pro	Gly	Glu	Cys	Phe	Gly	Leu	Leu
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Gly	Val	Asn	Gly	Ala	Gly	Lys	Thr	Ser	Thr	Phe	Arg	Met	Val	Thr
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Gly	Asp	Thr	Leu	Ala	Ser	Arg	Gly	Glu	Ala	Val	Leu	Ala	Gly	His
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Ser	Val	Ala	Arg	Glu	Pro	Ser	Ala	Ala	His	Leu	Ser	Met	Gly	Tyr
				1895					1900					1905
Cys	Pro	Gln	Ser	Asp	Ala	Ile	Phe	Glu	Leu	Leu	Thr	Gly	Arg	Glu
				1910					1915					1920
His	Leu	Glu	Leu	Leu	Ala	Arg	Leu	Arg	Gly	Val	Pro	Glu	Ala	Gln
				1925					1930					1935
Val	Ala	Gln	Thr	Ala	Gly	Ser	Gly	Leu	Ala	Arg	Leu	Gly	Leu	Ser
				1940					1945					1950
Trp	Tyr	Ala	Asp	Arg	Pro	Ala	Gly	Thr	Tyr	Ser	Gly	Gly	Asn	Lys
				1955					1960					1965
Arg	Lys	Leu	Ala	Thr	Ala	Leu	Ala	Leu	Val	Gly	Asp	Pro	Ala	Val

1970	1975	1980
Val Phe Leu Asp Glu	Pro Thr Thr Gly Met Asp	Pro Ser Ala Arg
1985	1990	1995
Arg Phe Leu Trp Asn	Ser Leu Leu Ala Val	Val Arg Glu Gly Arg
2000	2005	2010
Ser Val Met Leu Thr	Ser His Ser Met Glu	Glu Cys Glu Ala Leu
2015	2020	2025
Cys Ser Arg Leu Ala	Ile Met Val Asn Gly	Arg Phe Arg Cys Leu
2030	2035	2040
Gly Ser Pro Gln His	Leu Lys Gly Arg Phe	Ala Ala Gly His Thr
2045	2050	2055
Leu Thr Leu Arg Val	Pro Ala Ala Arg Ser	Gln Pro Ala Ala Ala
2060	2065	2070
Phe Val Ala Ala Glu	Phe Pro Gly Ala Glu	Leu Arg Glu Ala His
2075	2080	2085
Gly Gly Arg Leu Arg	Phe Gln Leu Pro Pro	Gly Gly Arg Cys Ala
2090	2095	2100
Leu Ala Arg Val Phe	Gly Glu Leu Ala Val	His Gly Ala Glu His
2105	2110	2115
Gly Val Glu Asp Phe	Ser Val Ser Gln Thr	Met Leu Glu Glu Val
2120	2125	2130
Phe Leu Tyr Phe Ser	Lys Asp Gln Gly Lys	Asp Glu Asp Thr Glu
2135	2140	2145
Glu Gln Lys Glu Ala	Gly Val Gly Val Asp	Pro Ala Pro Gly Leu
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Gln His Pro Lys Arg	Val Ser Gln Phe Leu	Asp Asp Pro Ser Thr
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Ala Glu Thr Val Leu		
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<221> misc_feature

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Leu Trp Ile Asn Lys	Pro Trp Val His Ser	Leu Leu Arg Ile Cys
35	40	45
Ala Ile Ile Ser Val	Ile Ser Val Cys Met	Asn Thr Pro Met Thr
50	55	60
Phe Glu His Tyr Pro	Pro Leu Gln Tyr Val	Thr Phe Thr Leu Asp
65	70	75
Thr Leu Leu Met Phe	Leu Tyr Thr Ala Glu	Met Ile Ala Lys Met
80	85	90
His Ile Arg Gly Ile	Val Lys Gly Asp Ser	Ser Tyr Val Lys Asp
95	100	105
Arg Trp Cys Val Phe	Asp Gly Phe Met Val	Phe Cys Leu Trp Val
110	115	120
Ser Leu Val Leu Gln	Val Phe Glu Ile Ala	Asp Ile Val Asp Gln
125	130	135
Met Ser Pro Trp Gly	Met Leu Arg Ile Pro	Arg Pro Leu Ile Met
140	145	150
Ile Arg Ala Phe Arg	Ile Tyr Phe Arg Phe	Glu Leu Pro Arg Thr
155	160	165
Arg Ile Thr Asn Ile	Leu Lys Arg Ser Gly	Glu Gln Ile Trp Ser
170	175	180
Val Ser Ile Phe Leu	Leu Phe Phe Leu Leu	Leu Tyr Gly Ile Leu
185	190	195
Gly Val Gln Met Phe	Gly Thr Phe Thr Tyr	His Cys Val Val Asn

Asp Thr Lys Pro	200	Asn Val Thr Trp	205	Asn Ser Leu Ala Ile	210
Asp Thr His Cys	215	Pro Glu Leu Glu	220	Gly Tyr Gln Cys	225
Pro Gly Phe Lys	230	Met Asp Leu Glu	235	Asp Leu Gly Leu Ser	240
Gln Glu Leu Gly	245	Tyr Ser Gly Phe Asn	250	Glu Ile Gly Thr Ser	255
Phe Thr Val Tyr	260	Glu Ala Ala Ser Gln	265	Gly Trp Val Phe	270
Met Tyr Arg Ala	275	Ile Asp Ser Phe Pro	280	Arg Trp Arg Ser Tyr	285
Tyr Phe Ile Thr	290	Leu Ile Phe Phe Leu	295	Ala Trp Leu Val Lys	300
Val Phe Ile Ala	305	Val Ile Ile Glu Thr	310	Phe Ala Glu Ile Arg	315
Gln Phe Gln Gln	320	Met Trp Gly Ser Arg	325	Ser Ser Thr Thr Ser	330
Ala Thr Thr Gln	335	Met Phe His Glu Asp	340	Ala Ala Gly Gly Trp	345
Leu Val Ala Val	350	Asp Val Asn Lys Pro	355	Gln Gly Arg Ala Pro	360
Cys Leu Gln Lys	365	Met Met Arg Ser Ser	370	Val Phe His Met Phe	375
Leu Ser Met Val	380	Thr Val Asp Val Ile	385	Val Ala Ala Ser Asn	390
Tyr Lys Gly Glu	395	Asn Phe Arg Arg Gln	400	Tyr Asp Glu Phe Tyr	405
Ala Glu Val Ala	410	Phe Thr Val Leu Phe	415	Asp Leu Glu Ala Leu	420
Lys Ile Trp Cys	425	Leu Gly Phe Thr Gly	430	Tyr Ile Ser Ser Ser	435
His Lys Phe Glu	440	Leu Leu Leu Val Ile	445	Gly Thr Thr Leu His	450
Tyr Pro Asp Leu	455	Tyr His Ser Gln Phe	460	Thr Tyr Phe Gln Val	465
Arg Val Val Arg	470	Leu Ile Lys Ile Ser	475	Pro Ala Leu Glu Asp	480
Val Tyr Lys Ile	485	Phe Gly Pro Gly Lys	490	Lys Leu Gly Ser Leu	495
Val Phe Thr Ala	500	Ser Leu Leu Ile Val	505	Met Ser Ala Ile Ser	510
Gln Met Phe Cys	515	Phe Val Glu Glu Leu	520	Asp Arg Phe Thr Thr	525
Pro Arg Ala Phe	530	Met Ser Met Phe Gln	535	Ile Leu Thr Gln Glu	540
Trp Val Asp Val	545	Met Asp Gln Thr Leu	550	Asn Ala Val Gly His	555
Trp Ala Pro Val	560	Val Ala Ile Tyr Phe	565	Ile Leu Tyr His Leu	570
Ala Thr Leu Ile	575	Leu Leu Ser Leu Phe	580	Val Ala Val Ile Leu	585
Asn Leu Glu Leu	590	Asp Glu Asp Leu Lys	595	Lys Leu Lys Gln Leu	600
Gln Ser Glu Ala	605	Asn Ala Asp Thr Lys	610	Glu Lys Leu Pro Leu	615
Leu Arg Ile Phe	620	Glu Lys Phe Pro Asn	625	Arg Pro Gln Met Val	630
Ile Ser Lys Leu	635	Pro Ser Asp Phe Thr	640	Val Pro Lys Ile Arg	645
Ser Phe Met Lys	650	Gln Phe Ile Asp Arg	655	Gln Gln Gln Asp Thr	660
Cys Leu Leu Arg	665	Ser Leu Pro Thr Thr	670	Ser Ser Ser Ser Cys	675
His Ser Lys Arg	680	Ser Ala Ile Glu Asp	685	Asn Lys Tyr Ile Asp	690
	695		700		705

Lys	Leu	Arg	Lys	Ser	Val	Phe	Ser	Ile	Arg	Ala	Arg	Asn	Leu	Leu	
				710					715					720	
Glu	Lys	Glu	Thr	Ala	Val	Thr	Lys	Ile	Leu	Arg	Ala	Cys	Thr	Arg	
				725					730					735	
Gln	Arg	Met	Leu	Ser	Gly	Ser	Phe	Glu	Gly	Gln	Pro	Ala	Lys	Glu	
				740					745					750	
Arg	Ser	Ile	Leu	Ser	Val	Gln	His	His	Ile	Arg	Gln	Glu	Arg	Arg	
				755					760					765	
Ser	Leu	Arg	His	Gly	Ser	Asn	Ser	Gln	Arg	Ile	Ser	Arg	Gly	Lys	
				770					775					780	
Ser	Leu	Glu	Thr	Leu	Thr	Gln	Asp	His	Cys	Asn	Thr	Val	Ile	Tyr	
				785					790					795	
Arg	Asn	Ala	Gln	Arg	Glu	Val	Ser	Glu	Ile	Lys	Met	Ile	Gln	Glu	
				800					805					810	
Lys	Lys	Glu	Leu	Ala	Glu	Met	Leu	Gln	Gly	Lys	Cys	Lys	Lys	Glu	
				815					820					825	
Leu	Arg	Glu	Ser	His	Pro	Tyr	Phe	Asp	Lys	Pro	Leu	Phe	Ile	Val	
				830					835					840	
Gly	Arg	Glu	His	Arg	Phe	Arg	Asn	Phe	Cys	Arg	Val	Val	Val	Arg	
				845					850					855	
Ala	Arg	Phe	Asn	Ala	Ser	Lys	Thr	Asp	Pro	Val	Thr	Gly	Ala	Val	
				860					865					870	
Lys	Asn	Thr	Lys	Tyr	His	Leu	Leu	Tyr	Asp	Leu	Leu	Gly	Leu	Val	
				875					880					885	
Thr	Tyr	Leu	Asp	Trp	Val	Met	Ile	Ile	Val	Thr	Ser	Asp	Ser	Cys	
				890					895					900	
Ile	Ser	Met	Met	Phe	Glu	Ser	Pro	Phe	Arg	Arg	Val	Met	His	Ala	
				905					910					915	
Pro	Thr	Leu	Gln	Ile	Ala	Glu	Tyr	Val	Phe	Val	Ile	Phe	Met	Ser	
				920					925					930	
Ile	Glu	Leu	Asn	Leu	Lys	Ile	Met	Ala	Asp	Gly	Leu	Phe	Phe	Thr	
				935					940					945	
Pro	Thr	Ala	Val	Ile	Arg	Asp	Phe	Gly	Gly	Val	Met	Asp	Ile	Phe	
				950					955					960	
Ile	Tyr	Leu	Val	Ser	Leu	Ile	Phe	Leu	Cys	Trp	Met	Pro	Gln	Asn	
				965					970					975	
Val	Pro	Ala	Glu	Ser	Gly	Ala	Gln	Leu	Leu	Met	Val	Leu	Arg	Cys	
				980					985					990	
Leu	Arg	Pro	Leu	Arg	Ile	Phe	Lys	Leu	Val	Pro	Gln	Met	Arg	Lys	
				995					1000					1005	
Val	Val	Arg	Glu	Leu	Phe	Ser	Gly	Phe	Lys	Glu	Ile	Phe	Leu	Val	
				1010					1015					1020	
Ser	Ile	Leu	Leu	Thr	Leu	Met	Leu	Val	Phe	Ala	Ser	Phe	Gly		
				1025					1030					1035	
Val	Gln	Leu	Phe	Ala	Gly	Lys	Leu	Ala	Lys	Cys	Asn	Asp	Pro	Asn	
				1040					1045					1050	
Ile	Ile	Arg	Arg	Glu	Asp	Cys	Asn	Gly	Ile	Phe	Arg	Ile	Asn	Val	
				1055					1060					1065	
Ser	Val	Ser	Lys	Asn	Leu	Asn	Leu	Lys	Leu	Arg	Pro	Gly	Glu	Lys	
				1070					1075					1080	
Lys	Pro	Gly	Phe	Trp	Val	Pro	Arg	Val	Trp	Ala	Asn	Pro	Arg	Asn	
				1085					1090					1095	
Phe	Asn	Phe	Asp	Asn	Val	Gly	Asn	Ala	Met	Leu	Ala	Leu	Phe	Glu	
				1100					1105					1110	
Val	Leu	Ser	Leu	Lys	Gly	Trp	Val	Glu	Val	Arg	Asp	Val	Ile	Ile	
				1115					1120					1125	
His	Arg	Val	Gly	Pro	Ile	His	Gly	Ile	Tyr	Ile	His	Val	Phe	Val	
				1130					1135					1140	
Phe	Leu	Gly	Cys	Met	Ile	Gly	Leu	Thr	Leu	Phe	Val	Gly	Val	Val	
				1145					1150					1155	
Ile	Ala	Asn	Phe	Asn	Glu	Asn	Lys	Gly	Thr	Ala	Leu	Leu	Thr	Val	
				1160					1165					1170	
Asp	Gln	Arg	Arg	Trp	Glu	Asp	Leu	Lys	Ser	Arg	Leu	Lys	Ile	Ala	
				1175					1180					1185	
Gln	Pro	Leu	His	Leu	Pro	Pro	Arg	Pro	Asp	Asn	Asp	Gly	Phe	Arg	
				1190					1195					1200	
Ala	Lys	Met	Tyr	Asp	Ile	Thr	Gln	His	Pro	Phe	Phe	Lys	Arg	Thr	

1205	1210	1215
Ile Ala Leu Leu Val	Leu Ala Gln Ser Val	Leu Leu Ser Val Lys
1220	1225	1230
Trp Asp Val Glu Asp	Pro Val Thr Val Pro	Leu Ala Thr Met Ser
1235	1240	1245
Val Val Phe Thr Phe	Ile Phe Val Leu Glu	Val Thr Met Lys Ile
1250	1255	1260
Ile Ala Met Ser Pro	Ala Gly Phe Trp Gln	Ser Arg Arg Asn Arg
1265	1270	1275
Tyr Asp Leu Leu Val	Thr Ser Leu Gly Val	Val Trp Val Val Leu
1280	1285	1290
His Phe Ala Leu Leu	Asn Ala Tyr Thr Tyr	Met Met Gly Ala Cys
1295	1300	1305
Val Ile Val Phe Arg	Phe Phe Ser Ile Cys	Gly Lys His Val Thr
1310	1315	1320
Leu Lys Met Leu Leu	Leu Thr Val Val Val	Ser Met Tyr Lys Ser
1325	1330	1335
Phe Phe Ile Ile Val	Gly Met Phe Leu Leu	Leu Leu Cys Tyr Ala
1340	1345	1350
Phe Ala Gly Val Val	Leu Phe Gly Thr Val	Lys Tyr Gly Glu Asn
1355	1360	1365
Ile Asn Arg His Ala	Asn Phe Ser Ser Ala	Gly Lys Ala Ile Thr
1370	1375	1380
Val Leu Phe Arg Ile	Val Thr Gly Glu Asp	Trp Asn Lys Ile Met
1385	1390	1395
His Asp Cys Met Val	Gln Pro Pro Phe Cys	Thr Pro Asp Glu Phe
1400	1405	1410
Thr Tyr Trp Ala Thr	Asp Cys Gly Asn Tyr	Ala Gly Ala Leu Met
1415	1420	1425
Tyr Phe Cys Ser Phe	Tyr Val Ile Ile Ala	Tyr Ile Met Leu Asn
1430	1435	1440
Leu Leu Val Ala Ile	Ile Val Glu Asn Phe	Ser Leu Ile Tyr Ser
1445	1450	1455
Thr Glu Glu Asp Gln	Leu Leu Ser Tyr Asn	Asp Leu Arg His Phe
1460	1465	1470
Gln Ile Ile Trp Asn	Met Val Asp Asp Lys	Arg Glu Val Phe Pro
1475	1480	1485
Thr Phe Arg Val Lys	Phe Leu Leu Arg Leu	Leu Arg Gly Arg Leu
1490	1495	1500
Glu Val Asp Leu Asp	Lys Asp Lys Leu Leu	Phe Lys His Met Cys
1505	1510	1515
Tyr Glu Met Glu Arg	Leu His Asn Gly Gly	Asp Val Thr Phe His
1520	1525	1530
Asp Val Leu Ser Met	Leu Ser Tyr Arg Ser	Val Asp Ile Arg Lys
1535	1540	1545
Ser Leu Gln Leu Glu	Leu Leu Leu Ala Arg	Glu Gln Leu Glu Tyr
1550	1555	1560
Thr Ile Glu Glu Glu	Val Ala Lys Gln Thr	Ile Arg Met Trp Leu
1565	1570	1575
Lys Lys Cys Leu Lys	Arg Ile Arg Ala Lys	Gln Gln Gln Ser Cys
1580	1585	1590
Ser Ile Ile His Ser	Leu Arg Glu Ser Gln	Gln Gln Glu Leu Ser
1595	1600	1605
Arg Phe Leu Asn Pro	Pro Ser Ile Glu Thr	Thr Gln Pro Ser Glu
1610	1615	1620
Asp Thr Asn Ala Asn	Ser Gln Asp Asn Ser	Met Gln Pro Glu Thr
1625	1630	1635
Ser Ser Gln Gln Gln	Leu Leu Ser Pro Thr	Leu Ser Asp Arg Gly
1640	1645	1650
Gly Ser Arg Gln Asp	Ala Ala Asp Ala Gly	Lys Pro Gln Arg Lys
1655	1660	1665
Phe Gly Gln Trp Arg	Leu Pro Ser Ala Pro	Lys Pro Ile Ser His
1670	1675	1680
Ser Val Ser Ser Val	Asn Leu Arg Phe Gly	Gly Arg Thr Thr Met
1685	1690	1695
Lys Ser Val Val Cys	Lys Met Asn Pro Met	Thr Asp Ala Ala Ser
1700	1705	1710

Cys	Gly	Ser	Glu	Val	Lys	Lys	Trp	Trp	Thr	Arg	Gln	Leu	Thr	Val
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Glu	Ser	Asp	Glu	Ser	Gly	Asp	Asp	Leu	Leu	Asp	Ile			
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<213> Homo sapiens

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<223> Incyte ID No: 168827CD1

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Phe	Gln	Ile	Leu	Gln	Met	Val	Phe	Leu	Ile	Met	Phe	Asn	Val	Ile
				20					25					30
Val	Tyr	His	Gln	Thr	Gln	Leu	Glu	Asn	Phe	Ala	Ala	Phe	Ile	Leu
				35					40					45
Asp	His	Arg	Cys	Trp	Val	His	Ile	Leu	Asp	Asn	Asp	Thr	Ile	Pro
				50					55					60
Asp	Asn	Asp	Pro	Gly	Thr	Leu	Ser	Gln	Asp	Ala	Leu	Leu	Arg	Ile
				65					70					75
Ser	Ile	Pro	Phe	Asp	Ser	Asn	Leu	Arg	Pro	Glu	Lys	Cys	Arg	Arg
				80					85					90
Phe	Val	His	Pro	Gln	Trp	Lys	Leu	Ile	His	Leu	Asn	Gly	Thr	Phe
				95					100					105
Pro	Asn	Thr	Ser	Glu	Pro	Asp	Thr	Glu	Pro	Cys	Val	Asp	Gly	Trp
				110					115					120
Val	Tyr	Asp	Gln	Ser	Ser	Phe	Pro	Ser	Thr	Ile	Val	Thr	Lys	Trp
				125					130					135
Asp	Leu	Val	Cys	Glu	Ser	Gln	Pro	Leu	Asn	Ser	Val	Ala	Lys	Phe
				140					145					150
Leu	Phe	Met	Ala	Gly	Met	Met	Val	Gly	Gly	Asn	Leu	Tyr	Gly	His
				155					160					165
Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Phe	Val	Leu	Arg	Trp	Ser	Tyr
				170					175					180
Leu	Gln	Leu	Ala	Ile	Val	Gly	Thr	Cys	Ala	Ala	Phe	Ala	Pro	Thr
				185					190					195
Ile	Leu	Val	Tyr	Cys	Ser	Leu	Arg	Phe	Leu	Ala	Gly	Ala	Ala	Thr
				200					205					210
Phe	Ser	Ile	Ile	Val	Asn	Thr	Val	Leu	Leu	Ile	Val	Glu	Trp	Ile
				215					220					225
Thr	His	Gln	Phe	Cys	Ala	Met	Ala	Leu	Thr	Leu	Thr	Leu	Cys	Ala
				230					235					240
Ala	Ser	Ile	Gly	His	Ile	Thr	Leu	Gly	Ser	Leu	Ala	Phe	Val	Ile
				245					250					255
Arg	Asp	Gln	Cys	Ile	Leu	Gln	Leu	Val	Met	Ser	Ala	Pro	Cys	Phe
				260					265					270
Val	Phe	Phe	Leu	Phe	Ser	Arg	Trp	Leu	Ala	Glu	Ser	Ala	Arg	Trp
				275					280					285
Leu	Ile	Ile	Asn	Asn	Lys	Pro	Glu	Glu	Gly	Leu	Lys	Glu	Leu	Thr
				290					295					300
Lys	Ala	Ala	His	Arg	Asn	Gly	Met	Lys	Asn	Ala	Glu	Asp	Ile	Leu
				305					310					315
Thr	Met	Glu	Val	Leu	Lys	Ser	Thr	Met	Lys	Gln	Glu	Leu	Glu	Ala
				320					325					330
Ala	Gln	Lys	Lys	His	Ser	Leu	Cys	Glu	Leu	Leu	Arg	Ile	Pro	Asn
				335					340					345
Ile	Cys	Lys	Arg	Ile	Cys	Phe	Leu	Ser	Phe	Val	Arg	Phe	Ala	Ser
				350					355					360
Thr	Ile	Pro	Phe	Trp	Gly	Leu	Thr	Leu	His	Leu	Gln	His	Leu	Gly
				365					370					375
Asn	Asn	Val	Phe	Leu	Leu	Gln	Thr	Leu	Phe	Gly	Ala	Val	Thr	Leu
				380					385					390

Leu	Ala	Asn	Cys	Val	Ala	Pro	Trp	Ala	Leu	Asn	His	Met	Ser	Arg
				395					400					405
Arg	Leu	Ser	Gln	Met	Leu	Leu	Met	Phe	Leu	Leu	Ala	Thr	Cys	Leu
				410					415					420
Leu	Ala	Ile	Ile	Phe	Val	Pro	Gln	Glu	Met	Gln	Thr	Leu	Arg	Val
				425					430					435
Val	Leu	Ala	Thr	Leu	Gly	Val	Gly	Ala	Ala	Ser	Leu	Gly	Ile	Thr
				440					445					450
Cys	Ser	Thr	Ala	Gln	Glu	Asn	Glu	Leu	Ile	Pro	Ser	Ile	Ile	Arg
				455					460					465
Gly	Arg	Ala	Thr	Gly	Ile	Thr	Gly	Asn	Phe	Ala	Asn	Ile	Gly	Gly
				470					475					480
Ala	Leu	Ala	Ser	Leu	Met	Met	Ile	Leu	Ser	Ile	Tyr	Ser	Arg	Pro
				485					490					495
Leu	Pro	Trp	Ile	Ile	Tyr	Gly	Val	Phe	Ala	Ile	Leu	Ser	Gly	Leu
				500					505					510
Val	Val	Leu	Leu	Leu	Pro	Glu	Thr	Arg	Asn	Gln	Pro	Leu	Leu	Asp
				515					520					525
Ser	Ile	Gln	Asp	Val	Glu	Asn	Glu	Gly	Val	Asn	Ser	Leu	Ala	Ala
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Pro	Gln	Arg	Ser	Ser	Val	Leu								
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<213> Homo sapiens

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<223> Incyte ID No: 7472734CD1

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Phe	Gln	Ile	Cys	Leu	Ile	Ala	Phe	Phe	Cys	Ile	Thr	Asn	Ile	Leu
				20					25					30
Leu	Phe	Pro	Asn	Ile	Val	Leu	Glu	Asn	Phe	Thr	Ala	Phe	Thr	Pro
				35					40					45
Ser	His	Arg	Cys	Trp	Val	Pro	Leu	Leu	Asp	Asn	Asp	Thr	Val	Ser
				50					55					60
Asp	Asn	Asp	Thr	Gly	Thr	Leu	Ser	Lys	Asp	Asp	Leu	Leu	Arg	Ile
				65					70					75
Ser	Ile	Pro	Leu	Asp	Ser	Asn	Leu	Arg	Pro	Gln	Lys	Cys	Gln	Arg
				80					85					90
Phe	Ile	His	Pro	Gln	Trp	Gln	Leu	Leu	His	Leu	Asn	Gly	Thr	Phe
				95					100					105
Pro	Asn	Thr	Asn	Glu	Pro	Asp	Thr	Glu	Pro	Cys	Val	Asp	Gly	Trp
				110					115					120
Val	Tyr	Asp	Arg	Ser	Ser	Phe	Leu	Ser	Thr	Ile	Val	Thr	Glu	Trp
				125					130					135
Asp	Leu	Val	Cys	Glu	Ser	Gln	Ser	Leu	Lys	Ser	Met	Val	Gln	Ser
				140					145					150
Leu	Phe	Met	Ala	Gly	Ser	Leu	Leu	Gly	Gly	Leu	Ile	Tyr	Gly	His
				155					160					165
Leu	Ser	Asp	Arg	Phe	Gly	Arg	Lys	Phe	Val	Leu	Arg	Trp	Ser	Tyr
				170					175					180
Leu	Gln	Leu	Ala	Ile	Val	Gly	Thr	Cys	Ala	Ala	Phe	Ala	Pro	Thr
				185					190					195
Ile	Leu	Val	Tyr	Cys	Ser	Leu	Arg	Phe	Leu	Ala	Gly	Ala	Ala	Thr
				200					205					210
Phe	Ser	Ile	Ile	Val	Asn	Thr	Val	Leu	Leu	Ile	Val	Glu	Trp	Ile
				215					220					225
Thr	His	Gln	Phe	Cys	Ala	Met	Ala	Leu	Thr	Leu	Thr	Leu	Cys	Ala
				230					235					240
Ala	Ser	Ile	Gly	His	Ile	Thr	Leu	Gly	Ser	Leu	Ala	Phe	Val	Ile
				245					250					255

Arg	Asp	Gln	Cys	Ile	Leu	Gln	Leu	Val	Met	Ser	Ala	Pro	Cys	Phe	
				260					265					270	
Val	Phe	Phe	Leu	Phe	Ser	Arg	Trp	Leu	Ala	Glu	Ser	Ala	Arg	Trp	
				275					280					285	
Leu	Ile	Ile	Asn	Asn	Lys	Pro	Glu	Glu	Gly	Leu	Lys	Glu	Leu	Arg	
				290					295					300	
Lys	Ala	Ala	His	Arg	Asn	Gly	Met	Lys	Asn	Ala	Glu	Asp	Ile	Leu	
				305					310					315	
Thr	Met	Glu	Val	Leu	Lys	Ser	Thr	Met	Lys	Gln	Glu	Leu	Glu	Ala	
				320					325					330	
Ala	Gln	Lys	Lys	His	Ser	Leu	Cys	Glu	Leu	Leu	Arg	Ile	Pro	Asn	
				335					340					345	
Ile	Cys	Lys	Arg	Ile	Cys	Phe	Leu	Ser	Phe	Val	Arg	Phe	Ala	Ser	
				350					355					360	
Thr	Ile	Pro	Phe	Trp	Gly	Leu	Thr	Leu	His	Leu	Gln	His	Leu	Gly	
				365					370					375	
Asn	Asn	Val	Phe	Leu	Leu	Gln	Thr	Leu	Phe	Gly	Ala	Val	Thr	Leu	
				380					385					390	
Leu	Ala	Asn	Cys	Val	Ala	Pro	Trp	Ala	Leu	Asn	His	Met	Ser	Arg	
				395					400					405	
Arg	Leu	Ser	Gln	Met	Leu	Leu	Met	Phe	Leu	Leu	Ala	Thr	Cys	Leu	
				410					415					420	
Leu	Ala	Ile	Ile	Phe	Val	Pro	Gln	Glu	Met	Gln	Thr	Leu	Arg	Val	
				425					430					435	
Val	Leu	Ala	Thr	Leu	Gly	Val	Gly	Ala	Ala	Ser	Leu	Gly	Ile	Thr	
				440					445					450	
Cys	Ser	Thr	Ala	Gln	Glu	Asn	Glu	Leu	Ile	Pro	Ser	Ile	Ile	Arg	
				455					460					465	
Gly	Arg	Ala	Thr	Gly	Ile	Thr	Gly	Asn	Phe	Ala	Asn	Ile	Gly	Gly	
				470					475					480	
Ala	Leu	Ala	Ser	Leu	Met	Met	Ile	Leu	Ser	Ile	Tyr	Ser	Arg	Pro	
				485					490					495	
Leu	Pro	Trp	Ile	Ile	Tyr	Gly	Val	Phe	Ala	Ile	Leu	Ser	Gly	Leu	
				500					505					510	
Val	Val	Leu	Leu	Leu	Pro	Glu	Thr	Arg	Asn	Gln	Pro	Leu	Leu	Asp	
				515					520					525	
Ser	Ile	Gln	Asp	Val	Glu	Asn	Glu	Gly	Val	Asn	Ser	Leu	Ala	Ala	
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Pro	Gln	Arg	Ser	Ser	Val	Leu									
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				20					25					30	
Gly	Asn	Ala	Gln	Ile	Val	Asp	Trp	Pro	Val	Val	Tyr	Ser	Asn	Asp	
				35					40					45	
Gly	Phe	Cys	Lys	Leu	Ser	Gly	Tyr	His	Arg	Ala	Asp	Val	Met	Gln	
				50					55					60	
Lys	Ser	Ser	Thr	Cys	Ser	Phe	Met	Tyr	Gly	Glu	Leu	Thr	Asp	Lys	
				65					70					75	
Lys	Thr	Ile	Glu	Lys	Val	Arg	Gln	Thr	Phe	Asp	Asn	Tyr	Glu	Ser	
				80					85					90	
Asn	Cys	Phe	Glu	Val	Leu	Leu	Tyr	Lys	Lys	Asn	Arg	Thr	Pro	Val	
				95					100					105	
Trp	Phe	Tyr	Met	Gln	Ile	Ala	Pro	Ile	Arg	Asn	Glu	His	Glu	Lys	
				110					115					120	

Val	Val	Leu	Phe	Leu	Cys	Thr	Phe	Lys	Asp	Ile	Thr	Leu	Phe	Lys
				125					130					135
Gln	Pro	Ile	Glu	Asp	Asp	Ser	Thr	Lys	Gly	Trp	Thr	Lys	Phe	Ala
				140					145					150
Arg	Leu	Thr	Arg	Ala	Leu	Thr	Asn	Ser	Arg	Ser	Val	Leu	Gln	Gln
				155					160					165
Leu	Thr	Pro	Met	Asn	Lys	Thr	Glu	Val	Val	His	Lys	His	Ser	Arg
				170					175					180
Leu	Ala	Glu	Val	Leu	Gln	Leu	Gly	Ser	Asp	Ile	Leu	Pro	Gln	Tyr
				185					190					195
Lys	Gln	Glu	Ala	Pro	Lys	Thr	Pro	Pro	His	Ile	Ile	Leu	His	Tyr
				200					205					210
Cys	Ala	Phe	Lys	Thr	Thr	Trp	Asp	Trp	Val	Ile	Leu	Ile	Leu	Thr
				215					220					225
Phe	Tyr	Thr	Ala	Ile	Met	Val	Pro	Tyr	Asn	Val	Ser	Phe	Lys	Thr
				230					235					240
Lys	Gln	Asn	Asn	Ile	Ala	Trp	Leu	Val	Leu	Asp	Ser	Val	Val	Asp
				245					250					255
Val	Ile	Phe	Leu	Val	Asp	Ile	Val	Leu	Asn	Phe	His	Thr	Thr	Phe
				260					265					270
Val	Gly	Pro	Gly	Gly	Glu	Val	Ile	Ser	Asp	Pro	Lys	Leu	Ile	Arg
				275					280					285
Met	Asn	Tyr	Leu	Lys	Thr	Trp	Phe	Val	Ile	Asp	Leu	Leu	Ser	Cys
				290					295					300
Leu	Pro	Tyr	Asp	Ile	Ile	Asn	Ala	Phe	Glu	Asn	Val	Asp	Glu	Gly
				305					310					315
Ile	Ser	Ser	Leu	Phe	Ser	Ser	Leu	Lys	Val	Val	Arg	Leu	Leu	Arg
				320					325					330
Leu	Gly	Arg	Val	Ala	Arg	Lys	Leu	Asp	His	Tyr	Leu	Glu	Tyr	Gly
				335					340					345
Ala	Ala	Val	Leu	Val	Leu	Leu	Val	Cys	Val	Phe	Gly	Leu	Val	Ala
				350					355					360
His	Trp	Leu	Ala	Cys	Ile	Trp	Tyr	Ser	Ile	Gly	Asp	Tyr	Glu	Val
				365					370					375
Ile	Asp	Glu	Val	Thr	Asn	Thr	Ile	Gln	Ile	Asp	Ser	Trp	Leu	Tyr
				380					385					390
Gln	Leu	Ala	Leu	Ser	Ile	Gly	Thr	Pro	Tyr	Arg	Tyr	Asn	Thr	Ser
				395					400					405
Ala	Gly	Ile	Trp	Glu	Gly	Gly	Pro	Ser	Lys	Asp	Ser	Leu	Tyr	Val
				410					415					420
Ser	Ser	Leu	Tyr	Phe	Thr	Met	Thr	Ser	Leu	Thr	Thr	Ile	Gly	Phe
				425					430					435
Gly	Asn	Ile	Ala	Pro	Thr	Thr	Asp	Val	Glu	Lys	Met	Phe	Ser	Val
				440					445					450
Ala	Met	Met	Met	Val	Gly	Ala	Leu	Leu	Tyr	Ala	Thr	Ile	Phe	Gly
				455					460					465
Asn	Val	Thr	Thr	Ile	Phe	Gln	Gln	Met	Tyr	Ala	Asn	Thr	Asn	Arg
				470					475					480
Tyr	His	Glu	Met	Leu	Asn	Asn	Val	Arg	Asp	Phe	Leu	Lys	Leu	Tyr
				485					490					495
Gln	Val	Pro	Lys	Gly	Leu	Ser	Glu	Arg	Val	Met	Asp	Tyr	Ile	Val
				500					505					510
Ser	Thr	Trp	Ser	Met	Ser	Lys	Gly	Ile	Asp	Thr	Glu	Lys	Val	Leu
				515					520					525
Ser	Ile	Cys	Pro	Lys	Asp	Met	Arg	Ala	Asp	Ile	Cys	Val	His	Leu
				530					535					540
Asn	Arg	Lys	Val	Phe	Asn	Glu	His	Pro	Ala	Phe	Arg	Leu	Ala	Ser
				545					550					555
Asp	Gly	Cys	Leu	Arg	Ala	Leu	Ala	Val	Glu	Phe	Gln	Thr	Ile	His
				560					565					570
Cys	Ala	Pro	Gly	Asp	Leu	Ile	Tyr	His	Ala	Gly	Glu	Ser	Val	Asp
				575					580					585
Ala	Leu	Cys	Phe	Val	Val	Ser	Gly	Ser	Leu	Glu	Val	Ile	Gln	Asp
				590					595					600
Asp	Glu	Val	Val	Ala	Ile	Leu	Gly	Lys	Gly	Asp	Val	Phe	Gly	Asp
				605					610					615
Ile	Phe	Trp	Lys	Glu	Thr	Thr	Leu	Ala	His	Ala	Cys	Ala	Asn	Val

Arg Ala Leu Thr	620	Tyr Cys Asp Leu His	625	Ile Ile Lys Arg Glu	630
Leu Leu Lys Val	635	Leu Asp Phe Tyr Thr	640	Phe Ala Asn Ser	645
Ser Arg Asn Leu	650	Thr Leu Thr Cys Asn	655	Leu Arg Lys Arg Ile	660
Phe Arg Lys Ile	665	Ser Asp Val Lys Lys	670	Glu Glu Glu Glu Arg	675
Arg Gln Lys Asn	680	Glu Val Thr Leu Ser	685	Ile Pro Val Asp His	690
Val Arg Lys Leu	695	Phe Gln Lys Phe Lys	700	Gln Gln Lys Glu Leu	705
Asn Gln Gly Ser	710	Thr Gln Gly Asp Pro	715	Glu Arg Asn Gln Leu	720
Val Glu Ser Arg	725	Ser Leu Gln Asn Gly	730	Ala Ser Ile Thr Gly	735
Ser Val Val Thr	740	Val Ser Gln Ile Thr	745	Pro Ile Gln Thr Ser	750
Ala Tyr Val Lys	755	Thr Ser Glu Ser Leu	760	Lys Gln Asn Asn Arg	765
Ala Met Glu Leu	770	Lys Pro Asn Gly Gly	775	Ala Asp Gln Lys Cys	780
Lys Val Asn Ser	785	Pro Ile Arg Met Lys	790	Asn Gly Asn Gly Lys	795
Trp Leu Arg Leu	800	Lys Asn Asn Met Gly	805	Ala His Glu Glu Lys	810
Glu Asp Trp Asn	815	Asn Val Thr Lys Ala	820	Glu Ser Met Gly Leu	825
Ser Glu Asp Pro	830	Lys Ser Ser Asp Ser	835	Glu Asn Ser Val Thr	840
Asn Pro Leu Arg	845	Lys Thr Asp Ser Cys	850	Asp Ser Gly Ile Thr	855
Ser Asp Leu Arg	860	Leu Asp Lys Ala Gly	865	Glu Ala Arg Ser Pro	870
Glu His Ser Pro	875	Ile Gln Ala Asp Ala	880	Lys His Pro Phe Tyr	885
Ile Pro Glu Gln	890	Ala Leu Gln Thr Thr	895	Leu Gln Glu Val Lys	900
Glu Leu Lys Glu	905	Asp Ile Gln Leu Leu	910	Ser Cys Arg Met Thr	915
Leu Glu Lys Gln	920	Val Ala Glu Ile Leu	925	Lys Ile Leu Ser Glu	930
Ser Val Pro Gln	935	Ala Ser Ser Pro Lys	940	Lys Ile Leu Ser Glu	945
Val Pro Pro Gln	950	Ile Pro Cys Gln Asp	955	Ser Gln Met Pro Leu	960
Pro Glu Ser Pro	965	Glu Ser Asp Lys Asp	970	Ile Phe Ser Val Ser	975
	980		985	Glu Ile His Phe	

<210> 32

<211> 533

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477725CD1

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Leu Ile Pro His Ile	35	Leu Leu Glu Asn Phe	40	Ala Ala Ala Ile Pro	45
Gly His Arg Cys Trp		Val His Met Leu Asp		Asn Asn Thr Gly Ser	

	50		55		60
Gly Asn Glu Thr	Gly Ile Leu Ser Glu	Asp Ala Leu Leu Arg	Ile		
	65		70		75
Ser Ile Pro Leu	Asp Ser Asn Leu Arg	Pro Glu Lys Cys Arg	Arg		
	80		85		90
Phe Val His Pro	Gln Trp Gln Leu Leu	His Leu Asn Gly Thr	Ile		
	95		100		105
His Ser Thr Ser	Glu Ala Asp Thr Glu	Pro Cys Val Asp Gly	Trp		
	110		115		120
Val Tyr Asp Gln	Ser Tyr Phe Pro Ser	Thr Ile Val Thr Lys	Trp		
	125		130		135
Asp Leu Val Cys	Asp Tyr Gln Ser Leu	Lys Ser Val Val Gln	Phe		
	140		145		150
Leu Leu Leu Thr	Gly Met Leu Val Gly	Gly Ile Ile Gly Gly	His		
	155		160		165
Val Ser Asp Arg	Phe Gly Arg Arg Phe	Ile Leu Arg Trp Cys	Leu		
	170		175		180
Leu Gln Leu Ala	Ile Thr Asp Thr Cys	Ala Ala Phe Ala Pro	Thr		
	185		190		195
Phe Pro Val Tyr	Cys Val Leu Arg Phe	Leu Ala Gly Phe Ser	Ser		
	200		205		210
Met Ile Ile Ile	Ser Asn Asn Ser Leu	Pro Ile Thr Glu Trp	Ile		
	215		220		225
Arg Pro Asn Ser	Lys Ala Leu Val Val	Ile Leu Ser Ser Gly	Ala		
	230		235		240
Leu Ser Ile Gly	Gln Ile Ile Leu Gly	Gly Leu Ala Tyr Val	Phe		
	245		250		255
Arg Asp Trp Gln	Thr Leu His Val Val	Ala Ser Val Pro Phe	Phe		
	260		265		270
Val Phe Phe Leu	Leu Ser Arg Trp Leu	Val Glu Ser Ala Arg	Trp		
	275		280		285
Leu Ile Ile Thr	Asn Lys Leu Asp Glu	Gly Leu Lys Ala Leu	Arg		
	290		295		300
Lys Val Ala Arg	Thr Asn Gly Ile Lys	Asn Ala Glu Glu Thr	Leu		
	305		310		315
Asn Ile Glu Val	Val Arg Ser Thr Met	Gln Glu Glu Leu Asp	Ala		
	320		325		330
Ala Gln Thr Lys	Thr Val Cys Asp	Leu Phe Arg Asn Pro	Ser		
	335		340		345
Met Arg Lys Arg	Ile Cys Ile Leu Val	Phe Leu Arg Phe Ala	Asn		
	350		355		360
Thr Ile Pro Phe	Gly Thr Met Val	Asn Leu Gln His Val	Gly		
	365		370		375
Ser Asn Ile Phe	Leu Leu Gln Val Leu	Tyr Gly Ala Val Ala	Leu		
	380		385		390
Ile Val Arg Cys	Leu Ala Leu Leu Thr	Leu Asn His Met Gly	Arg		
	395		400		405
Arg Ile Ser Gln	Ile Leu Phe Met Phe	Leu Val Gly Leu Ser	Ile		
	410		415		420
Leu Ala Asn Thr	Phe Val Pro Lys Glu	Met Gln Thr Leu Arg	Val		
	425		430		435
Ala Leu Ala Cys	Leu Gly Ile Gly Cys	Ser Ala Ala Thr Phe	Ser		
	440		445		450
Ser Val Ala Val	His Phe Ile Glu Leu	Ile Pro Thr Val Leu	Arg		
	455		460		465
Ala Arg Ala Ser	Gly Ile Asp Leu Thr	Ala Ser Arg Ile Gly	Ala		
	470		475		480
Ala Leu Ala Pro	Leu Leu Met Thr Leu	Thr Val Phe Phe Thr	Thr		
	485		490		495
Leu Pro Trp Ile	Ile Tyr Gly Ile Phe	Pro Ile Ile Gly Gly	Leu		
	500		505		510
Ile Val Phe Leu	Leu Pro Glu Thr Lys	Asn Leu Pro Leu Pro	Asp		
	515		520		525
Thr Ile Lys Asp	Val Glu Asn Gln				
	530				

<210> 33

<211> 1775
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 3474673CB1

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gggcccagatg cccacagttc agagcctctt tttgtcccg ggattggatc ccagggtctgg 180
gtggggccag gctgtcccat tccccaacac tctctctccc cggcgaaacc gggcaccagc 240
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gcggctcccg agggcagggt ccggggctgc ggggtgccc gcaccgtgct cctgctgctc 420
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gcgaggact ccagccgcag cttccagcgc gacaagtggg agctgttgca gaacttcacg 540
tgtctggacc gcccgcgct ggactcgctg atccgggatg tcgtccaagc atacaaaaac 600
ggagccagcc tctcagcaa caccaccagc atggggcgct gggagctcgt gggctccttc 660
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tgtggcaagg acagctagtt ataactcatt ctttggtcgt cgtcctcggt agcaagacc 1380
ctgattttta gctttgcaca tgtccacca aactaaagac tacattttcc atccacccta 1440
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ccatgaagta gcgcaaatgt ttgagcggca caataagata ggaagagtct ggtctctga 1680
tgatcacaga gccatcctaa caaacggaat atcacccgac ctcttttatg tgagagagaa 1740
ataaacatct tatgtaaaaa accaaaaaaa aaaaa 1775

<210> 34
<211> 1545
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 4588877CB1

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cacgatggct gcccgctct tctgcatct ctttgcctt gtggggatcc cactcaacct 180
cgtggtgctc aaccgactgg ggcattctat gcagcaggga gtaaaccact gggccagcag 240
gctggggggc acctggcagg tgagggggct gctggacggg gtggggatgg gtcacttcta 300
gaatgagggg ctgtggtggg aattggggtt actaatgaca agaggtggga gcaagtgtta 360
ctggtgaggt tgtgttggga ttgggggtca ctgctcagaa tagggtcctt agtgaaaag 420
ggcattaatg gtggagatgg ggtgggactg ggcagacagg aaggacatga ggcacaggct 480
ccaggcaggg aacctggaga acacagacca ggtgaagagc ccccttctta ctggggacag 540
ctctggcctg cctccagctc cctcggtccc cagcatggg gtgaaggcct caggaggcct 600
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cgctgcaggc	tgtggcaagg	acagctagtt	atactccatt	ctttggctgt	cgctcctcgg	1140
agcaagaccc	ctgattttaa	gctttgcaca	tgccacacca	aactaaagac	tacattttcc	1200
atccacccta	gaggctgggt	gcagctatat	gattaattct	gccaatagg	gtatacagag	1260
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ccacttcctt	actttagcgg	gctgcaatgc	cgccgatatg	atggctggga	gctctggcag	1380
ccatacggca	ccatgaagta	gcggcaatgt	ttgagcggca	caataagata	ggaagagtct	1440
ggatctctga	tgatcacaga	gccatcctaa	caaacggaat	atcacccgac	ctcctttatg	1500
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<210> 35

<211> 1941

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7472214CB1

<400> 35

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gagaaccaca	tactgaagc	ccagcgttc	tcccacctac	ccaagcgctc	agcgtgggac	180
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tataagaccc	ttctcaagtg	cctctcaggt	aaattctgcc	gccgggagct	gattggcctc	300
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aagatgtcct	gctacatcat	gcaagatgac	atgctgctgc	cgcacctcac	ggtgttggaa	480
gccatgatgg	tgtctgctaa	cctgaatctt	actgagaatc	ccgatgtgaa	aaacgatctc	540
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ctctctggcg	ggcagaggaa	gggtctggcc	atcgccctgg	agctgggtcaa	caaccgcct	660
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aaccccatgt	gtttcagggc	tgtgcagaat	gggctgtgct	ctatggctga	gaagaagagc	1020
agccctgaga	agaacgaggt	ccctgcccc	tgccctcctt	gtcctccgga	agtggatccc	1080
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agccgcttcc	tgtcttctc	agccctggcc	accgccaccg	ccttgggtggc	ccaatctttg	1560
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<210> 36

<211> 4971

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7473053CB1

<400> 36

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ggcggggcgc	gagcgtgag	cgctgagggt	ctcccatggg	attgctggga	tcttctgtgg	180

tgagatggca	gtgtgtgcaa	aaaagcgccc	cccagaagaa	gaaaggaggg	cgcgggctaa	240
tgaccgagaa	tacaatgaga	aattccagta	tgccagtaac	tgcatcaaga	cctccaagta	300
caatattctc	accttcctgc	ctgtcaacct	ctttgagcag	ttccagggaag	ttgccaaacac	360
ttacttccctg	ttcctcctca	ttctgcagtt	gatccccag	atctcttccc	tgctctgggtt	420
caccaccatt	gtgccttttg	ttcttgtcct	caccatcaca	gctgttaaag	atgccactga	480
tgactatttc	cgccacaaga	gcgataacca	ggtgaataac	cgccagtcct	aggtgttgat	540
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gctgtgttac	atagagacag	cagaacttga	tgccgagacc	aacatgaaag	tacgtcaggc	720
gattccagtc	acctcagaat	tgggagacat	cagtaagctt	gccaaagttt	acggtgaagt	780
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<210> 41

<211> 2877

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 7477898CB1

<400> 41

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<210> 42

<211> 2820

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7472728CB1

<400> 42

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<210> 43
<211> 1440
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 7474322CB1

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<220>
<221> unsure
<222> 757
<223> a, t, c, g, or other

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<210> 44
<211> 2394
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 5455621CB1

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<210> 45

<211> 2890

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477248CB1

<400> 45

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<223> Incyte ID No: 2944004CB1

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<223> Incyte ID No: 4538363CB1

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<400> 49

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<223> Incyte ID No: 7474127CB1

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<212> DNA

<213> Homo sapiens

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<400> 52

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<223> Incyte ID No: 1471717CB1

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<220>

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<223> Incyte ID No: 4599654CB1

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